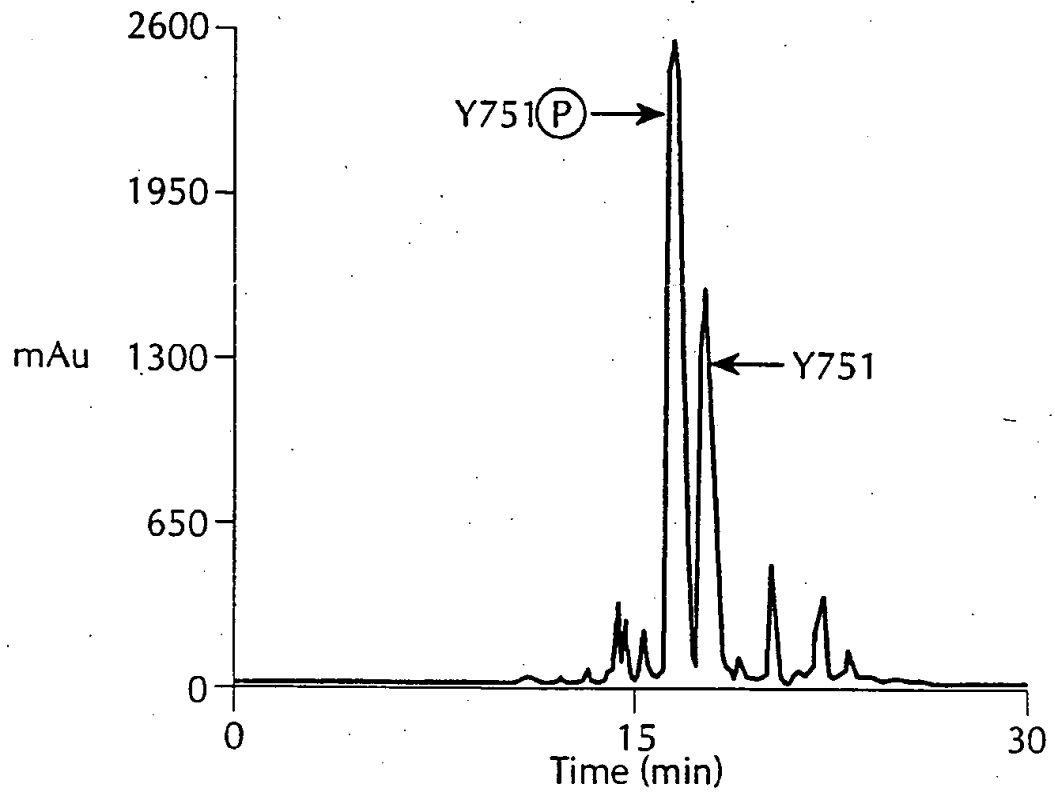
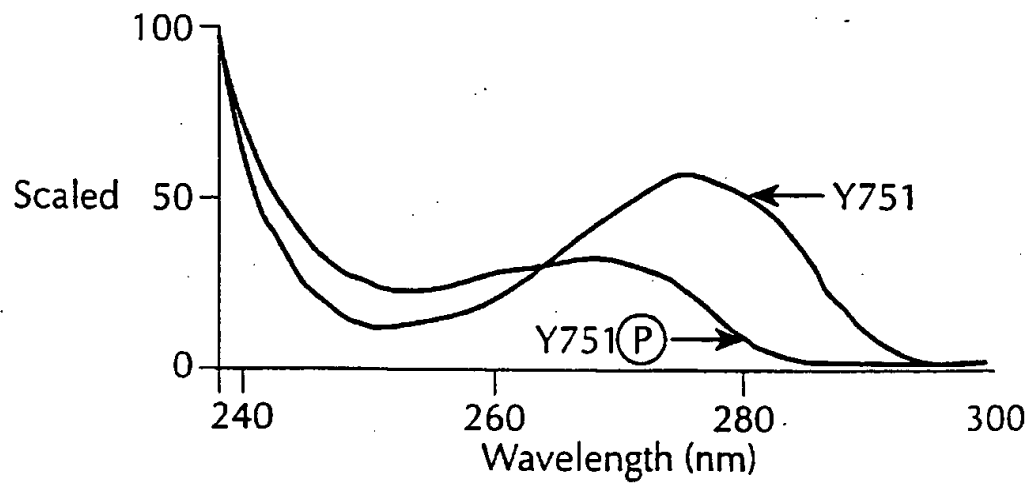




**FIG. 1A**



**FIG. 1B**



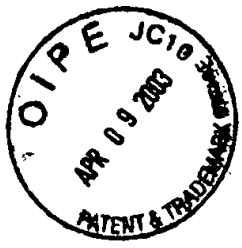


FIG. 1C

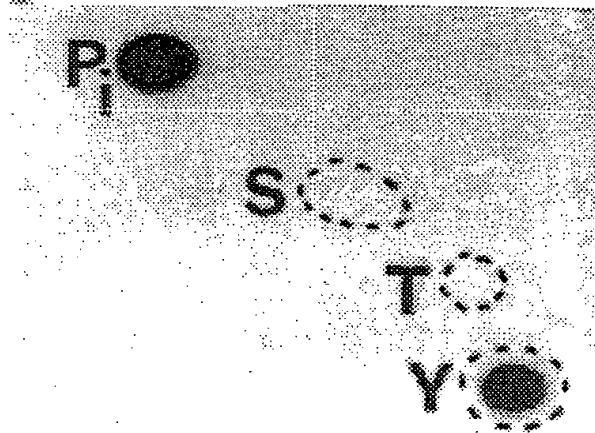
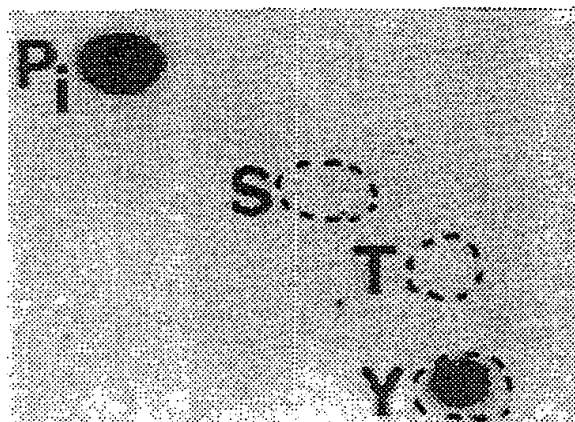


FIG. 1D



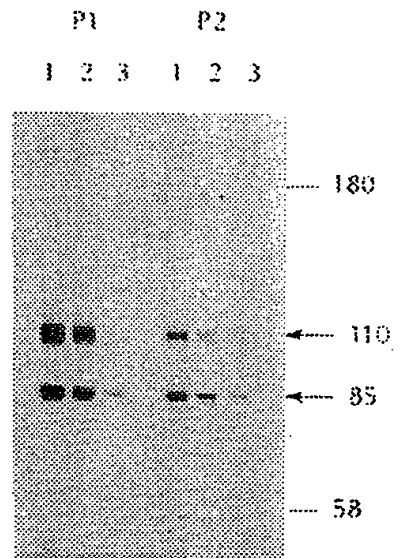
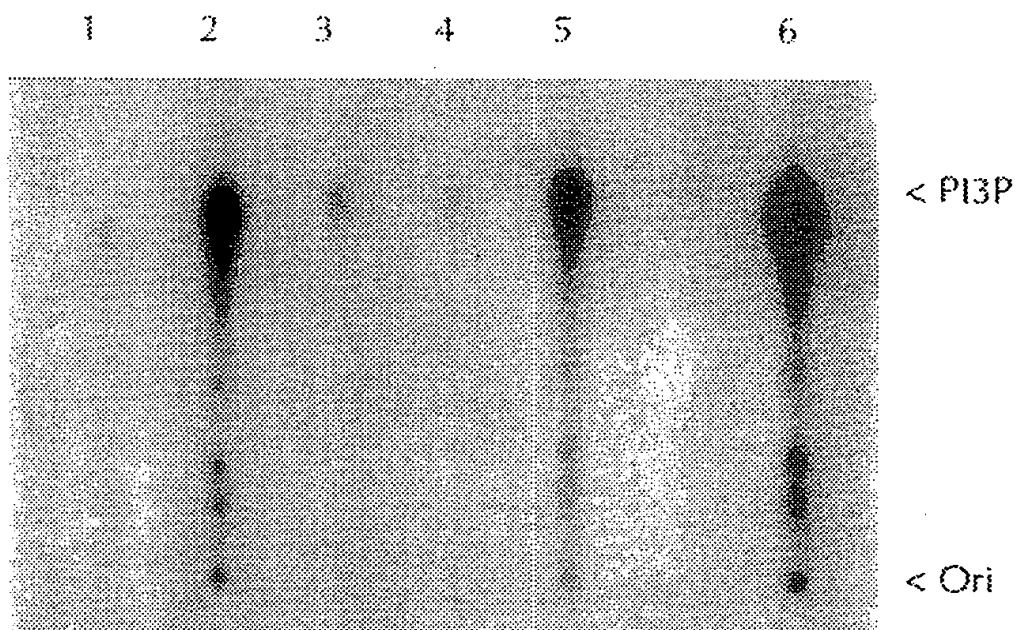




FIG. 3



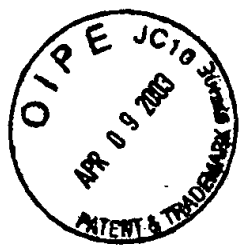
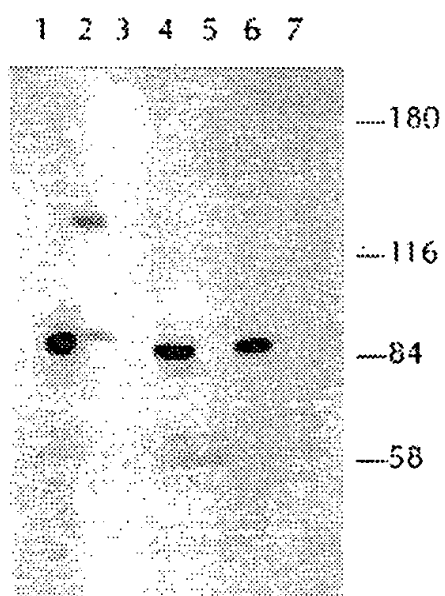
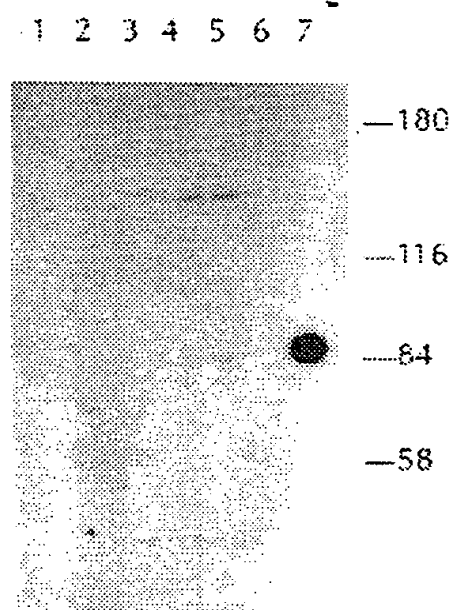


FIG. 4A

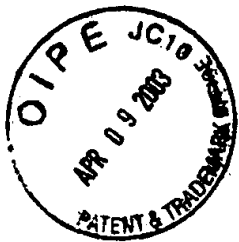


anti-ALPHA

FIG. 4B



anti-BETA



Official Patent  
Office of the  
United States Patent  
and Trademark Office

FIG. 4C

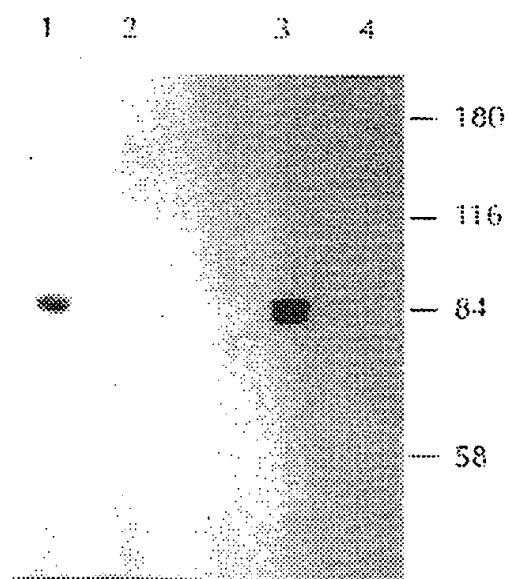


FIG. 4D

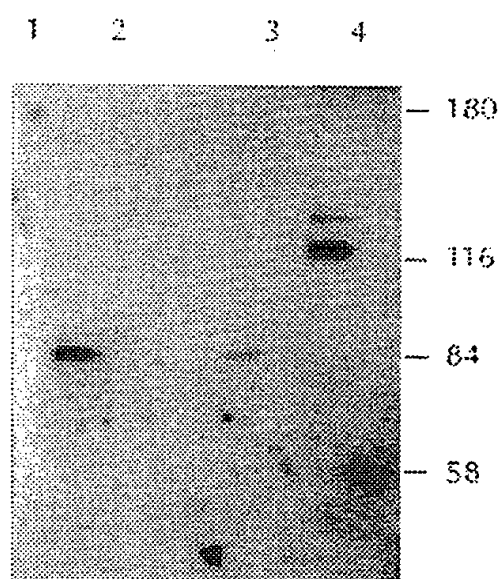




FIG. 5A

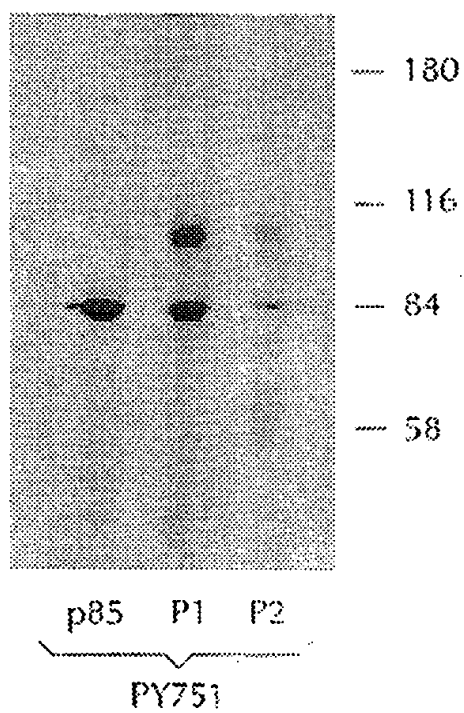


FIG. 5B

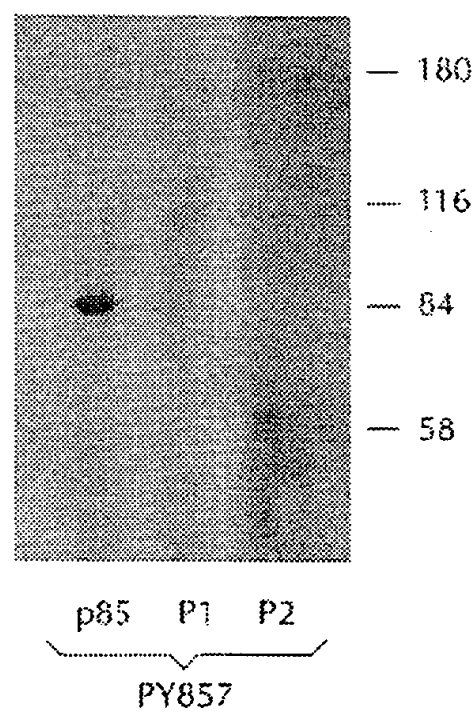




FIG. 6A

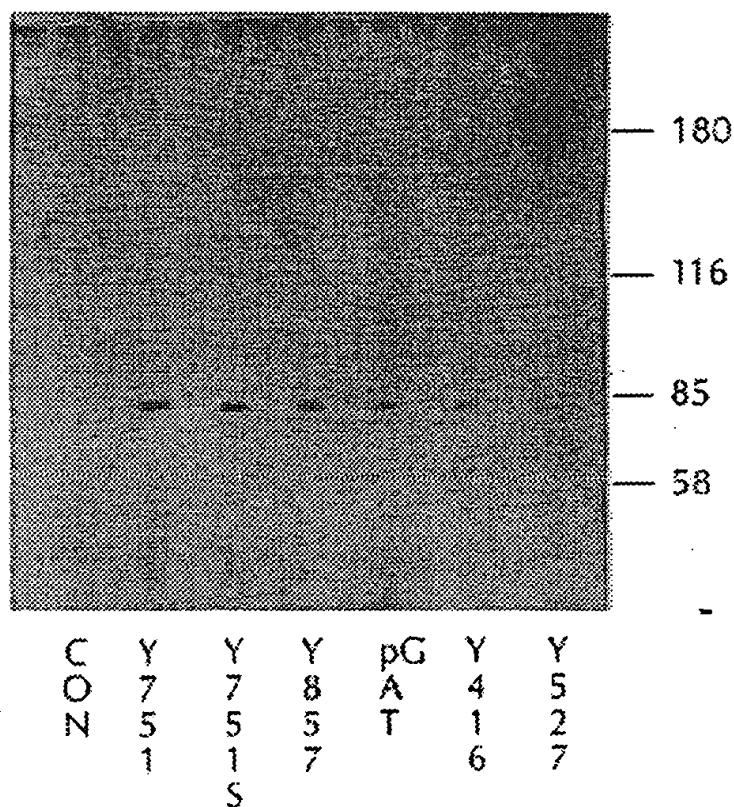
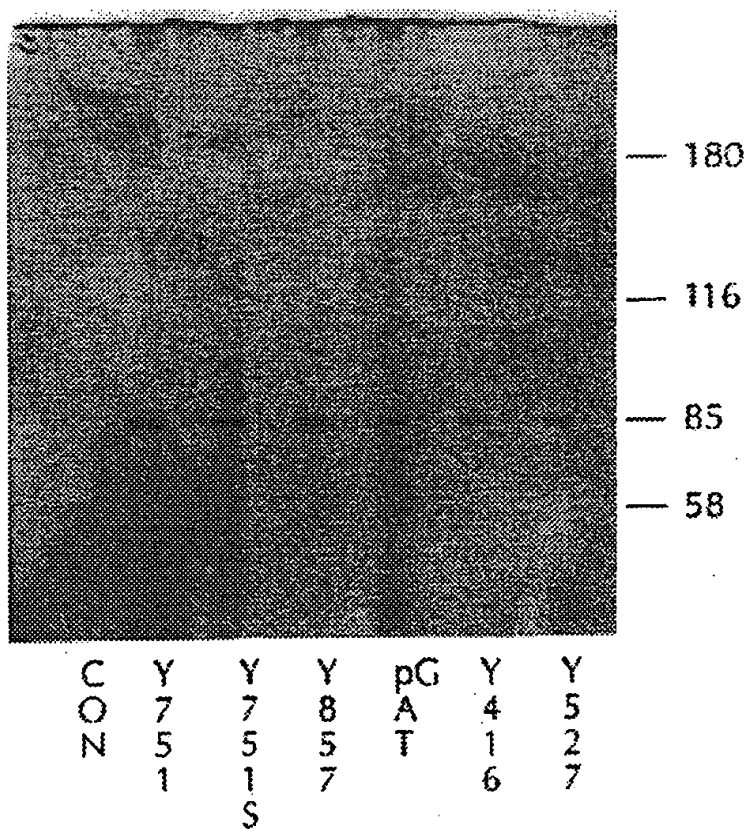


FIG. 6B





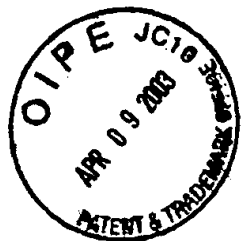


FIG. 7A

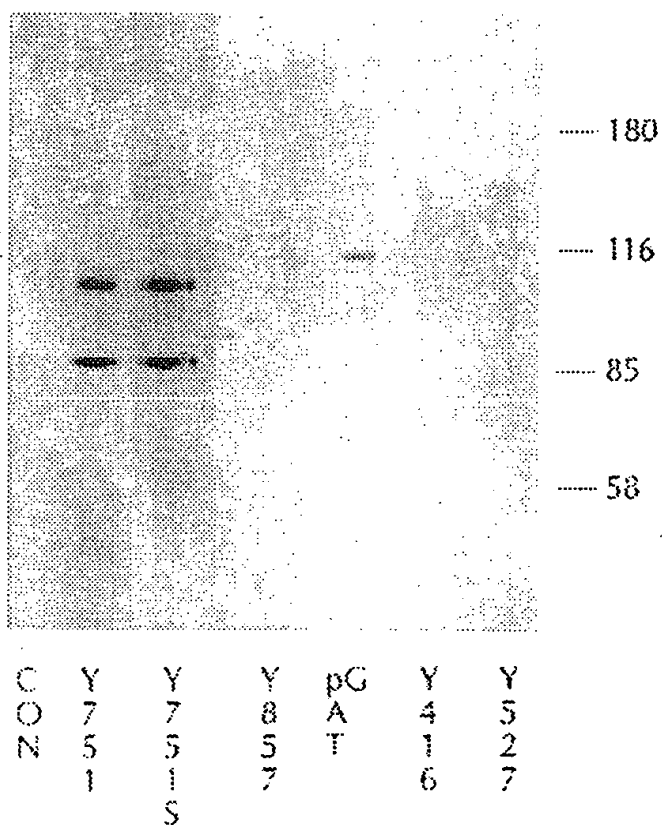


FIG. 7B

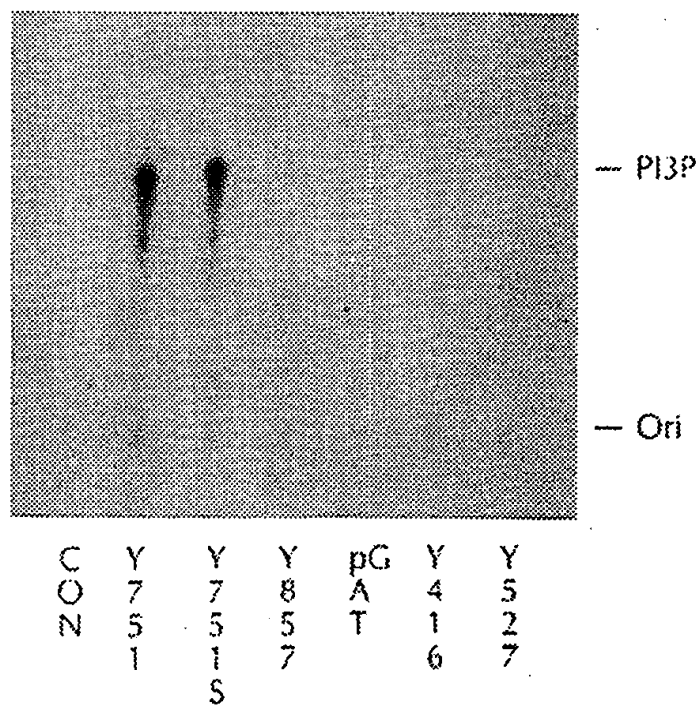




FIG. 8A

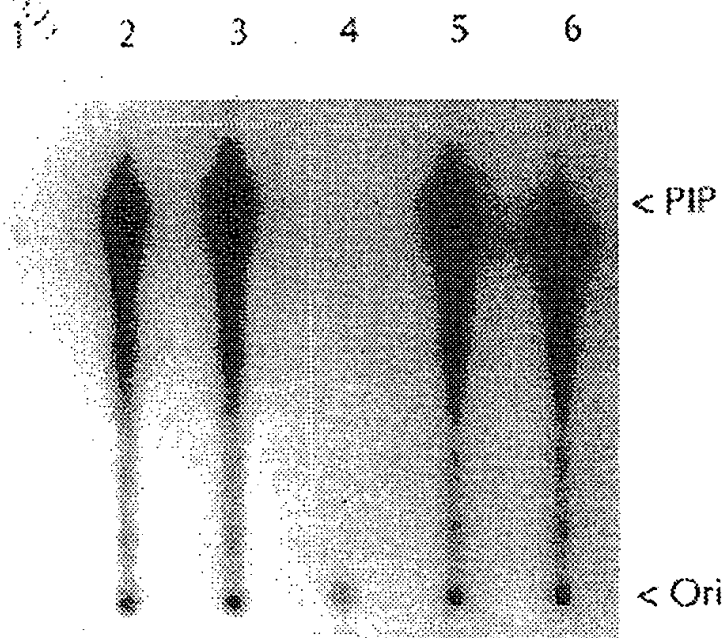


FIG. 8B

751	D M S K D E S V D Y V P M L D M K
751.S	C D E S V D Y V P M L
740	G E S D G G Y M D M S K
1313	E F C P D P L Y E V M L K
Consensus	E E E E E Y M P M X X
	D D D D D V



## FIG. 9A

M P P R P S S G E L W G I H L M 16  
ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 48

P P R I L V E C L L P N G M I V 32  
CCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTG 96

T L E C L R E A T L I T I K H E 48  
ACTTTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA 144

L F K E A R K Y P L H Q L L Q D 64  
CTATTTAAAGAAGCAAGAAAATACCCCTCTCCATCAACTTCTTCAAGAT 192

E S S Y I F V S V T Q E A E R E 80  
GAATCTTCTTACATTTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA 240

E F F D E T R R L C D L R L F Q 96  
GAATTTTTTGATGAAACAAGAAGACTTTGTGACCTTCGGCTTTTTTCAA 288

P F L K V I E P V G N R E E K I 112  
CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC 336

L N R E I G F A I G M P V C E F 128  
CTCAATCGAGAAATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTC 384

D M V K D P E V Q D F R R N I L 144  
GATATGGTTAAAGATCCAGAAGTACAGGACTTCGAAGAAATATTCTC 432



## FIG. 9B

N V C K E A V D L R D L N S P H 160  
AATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480  
A  
S R A M Y V Y P P N V E S S P E - 176  
AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAATCTTCACCAGAA 528  
L P K H I Y N K L D K G Q I I V 192  
CTGCCAAAGCACATATATAATAAATTGGATAAAGGGCAAATAATAGTG 576  
V I W V I V S P N N D K Q K Y T 208  
GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAACAGAAGTATACT 624  
L K I N H D C V P E Q V I A E A 224  
CTGAAAATCAACCATGACTGTGTGCCAGAACAGTAATTGCTGAAGCA 672  
I R K K T R S M L L S S E Q L K 240  
ATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAAA 720  
L C V L E Y Q G K Y I L K V C G 256  
CTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA 768  
C D E Y F L E K Y P L S Q Y K Y 272  
TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT 816  
I R S C I M L G R M P N L M L M 288  
ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGATGCTGATG 864





## FIG. 9D

T D T L V S G K M A L N L W P V 448  
ACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCITTGGOCAGTA 1344

C

P H G L E D L L N P I G V T G S 464  
CCTCATGGACTAGAAGATTGCTGAACCOCTATTGGTGTTACTGGATCA 1392

N P N K E T P C L E L E F D W F 480  
AATCCAAATAAAGAAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTC 1440

S S V V K F P D M S V I E E H A 496  
AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCC 1488

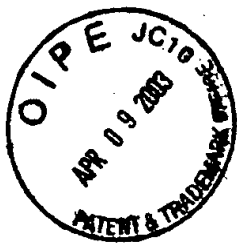
N W S V S R E A G F S Y S H A G 512  
AATTGGTCTGTATCCOGTGAAGCAGGATTTAGTTATTCCCATGCAGGA 1536

L S N R L A R D N E L R E N D K 528  
CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGAGAAAATGATAAA 1584

E Q L R A I C T R D P L S E I T 544  
GAACAGCTCOGAGCAATTTGTACACGAGATCCTCTATCTGAAATCACT 1632

E Q E K D F L W S H R H Y C V T 560  
GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTA ACT 1680

I P E I L P K L L L S V K W N S 576  
ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGA ACTCT 1728



## FIG. 9E

R D E V A Q M Y C L V K D W P P 592  
AGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGATTGGCCTCCA 1776

I K P E Q A M E L L D C N Y P D 608  
ATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGAT 1824

P M V R G F A V R C L E K Y L T 624  
CCTATGGITCGAGGTTTTGCTGTTGGTGCTTAGAAAAATATTTAACA 1872

D  
D D K L S O Y L I O L V O V L K 640  
GATGACAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAAA 1920

Y E O Y L D N L L V R F L L K K 656  
TATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAAA 1968

E  
A L T N O R I G H F F F W H L K 672  
GCGTTAACTAATCAAAGGATCGGTCACTTTTTCTTTTGGCATTAAAA 2016

F  
S E M H N K T V S O R F G L L L 688  
TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCITTTG 2064

E S Y C R A C G M Y L K H L N R 704  
GAGTCCTATTGCGTGTCATGTGGGATGTATCTGAAGCACCTTAATAGG 2112

G  
Q V E A M E K L I N L T D I L K 720  
CAAGTTGAGGCTATGGAAAAGCTCATTAACTTGACTGACATTCTCAA 2160



FIG. 9F

Q E K K D E T Q K V Q M K F L V 736  
CAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2208

E Q M R R P D F M D A L Q G F L 752  
GAGCAAATGOGGCGAACCAGATTTTCATGGATGCTCTCCAGGGCTTTCTG 2256

S P L N P A H Q L G N L R L E E 768  
TCTCCTCTAAACCOCTGCTCATCAGCTGGGAAATCTCAGGCITTGAAGAG 2304

C R I M S S A K R P L W L N W E 784  
TGTCGAATTATGTCTTCTGCAAAAAGGOCAGTGTGGTTGAATTGGGAG 2352

N P D I M S E L L F Q N N E I I 800  
AACCAGACATCATGTCAGAATTACTCTTTTCAGAACAAATGAGATCATC 2400

F K N G D D L R Q D M L T L Q I 816  
TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATT 2448

I R I M E N I W Q N Q G L D L R 832  
ATTGCAATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTGA 2496

M L P Y G C L S I G D C V G L I 848  
ATGTTAOCCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC 2544

E V V R N S H T I M Q I Q C K G 864  
GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCAAGTGTAAGGA 2592







FIG. 9H

Q H A N L F I N L F S M M L G S 1008  
CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT 3024

G M P E L Q S F D D I A Y I R K 1024  
GGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATTGAAAG 3072

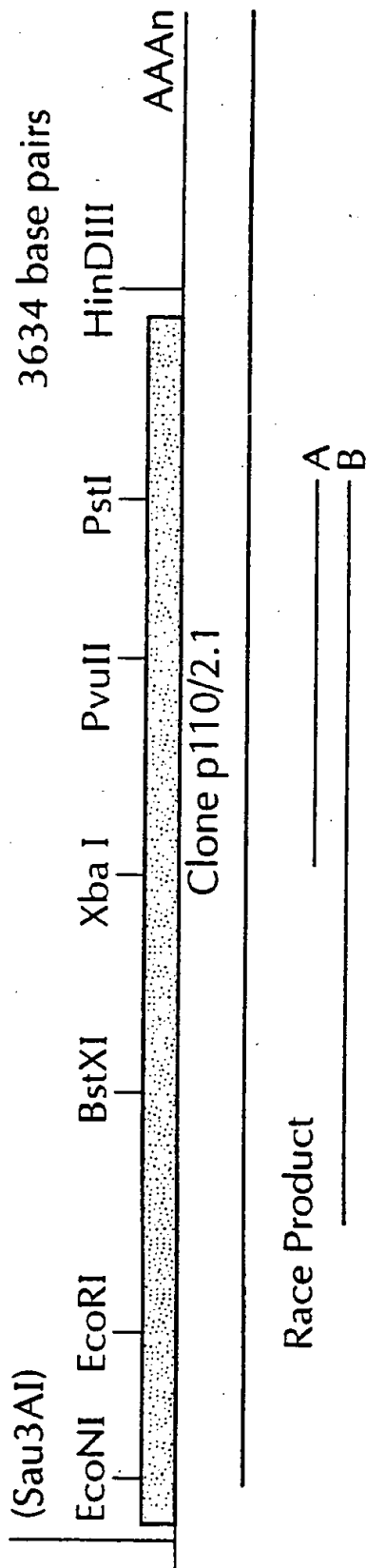
T L A L D K T E O E A L E Y F M 1040  
ACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG 3120

K Q M N D A H H G G W T T K M D 1056  
AAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAAATGGAT 3168

W I F H T I K Q H A L N \* 1069  
TGGATCTTCCACACAATTAAGCAGCATGCTTTGAACTGA 3207



**FIG. 9I**





**FIG. 10A**

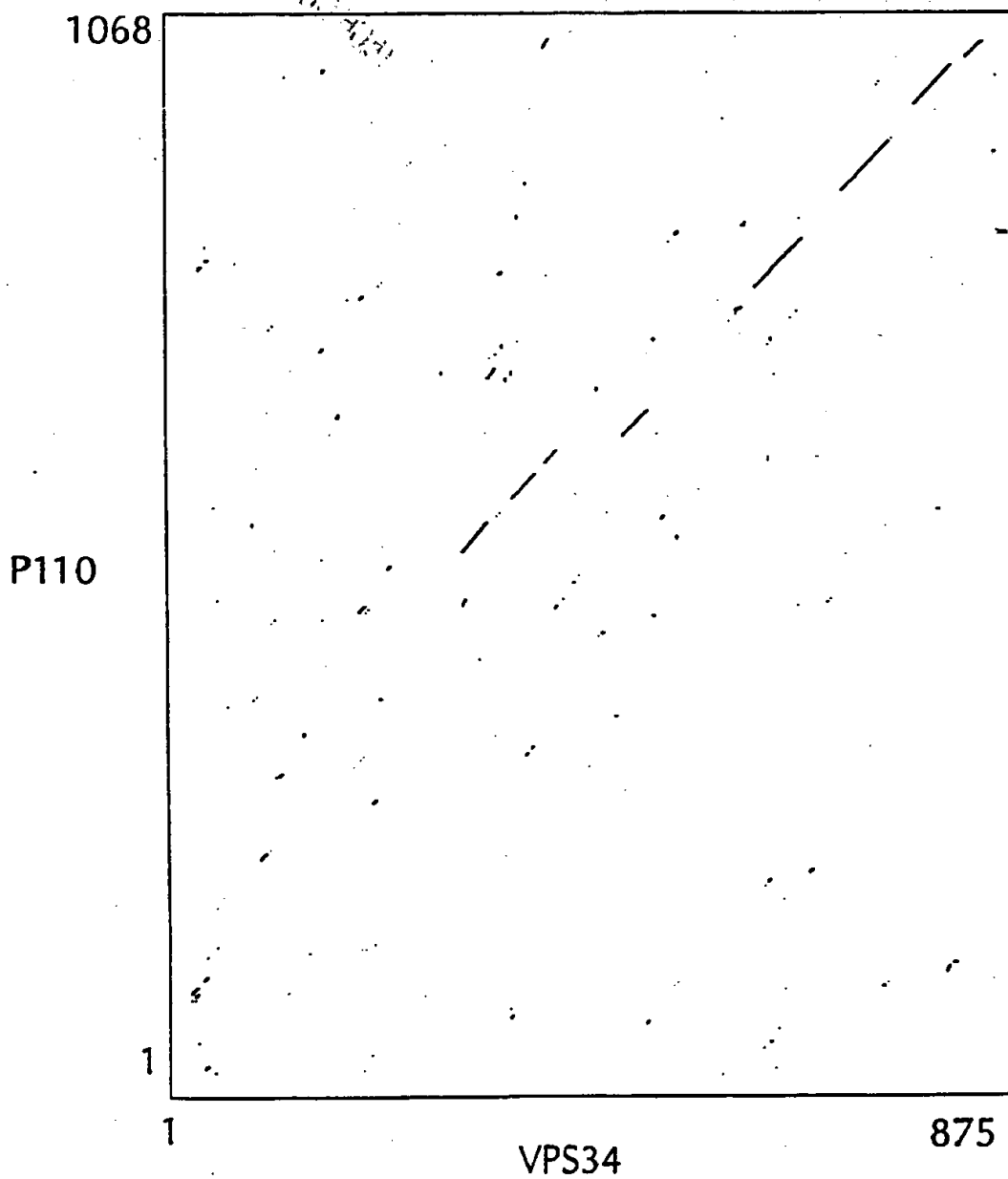




FIG. 10B

P110 VCEFDVVKDPEVQDFERNILNVCKEAVDLRDLNSPHSRAMYVYPPN 170  
..| :.| :|. :. :| :. :. :| :. .. :...| -  
VPS34 NITFCVSDQDLDVP.LKVKIKSLEGHKPLLKPSQKILNPEMLIGSN 49  
171 VESSPEL..PKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE 218  
|.|. :| :. :. :| :. :. :| :. | :. :. :. :.  
50 VEPSSDLIVSLQVFDKERNRNLTLPIYTPYIPFRNSRIWDYWL..... 92  
219 QVIAEAIRKKTRSMILSSEQLKLCVLEYQGYILKVCGCDEYFLEKYPLS 268  
... :. :. :. :|| :| :. :. :||. |  
93 .....TLPIRIKQLTFSS.HLRIILWEYNG..... 116  
269 QYKYIRSCIMLGRMPNIMLMAKESLYSQLPMDCFIMPSYSRRISTATPYM 318  
|...| :.  
117 .....SKQIPFF 123  
319 NGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC 368  
| |||. :. :. :. :| :| :. :. :| :. :. :| :.  
124 NLETSI..FNLKDCTLK.....RGFESLKFRYDVIDHCEVVT 158  
369 DNVNTQRVPCSNPRWNEWLNNDIYIPDLPRARLC.LSICSVKGRKGAKE 417  
|| : .| || :. :. :| :| :. :| :. :. :. :.  
159 DNKD.....QENLN.KYFQGEFTRLPWLDEITISKLRKQRENRT 196



418	.EHCPLAWG.NINLFDYDTLVS GKMAI NLWVPVPHGLEDLLNPIGV TGS.	464
	..... :: :::: .:: .: .: .:   .      :...	
197	WPOGTFVLNLEFPMLELPVVFIEREIMNTQMNIP....TLKNNPGLSTDL	242
	.....	
465	.NPNKETPCLELEF.DWFSSVVKFPDMSVIEEHANWSVSREAGE'SYSHAG	512
	:  :::  ::::  ::  ::     ::::  ..   :::: :	
243	REPNRNDPQIKISLGDKYHSTLKFYD....PDQPNNDPIEEKYRRLERAS	288
	.....	
513	LSNRLARDNELRENDKEQLRAICTRDPLSEITEQEKDFLWSHRHYCVTIP	562
	... ::: . ::::  .  .. .  .. ::  : : .. .   ..	
289	KNANLDKQVKPDIKKRDYLNKIINYPGTKLTAHEKGSWKYRYYIMNNK	338
	.....	
563	EILPKLLLSVKWNSRDEVAQMYCLVKDWPPIKEQAMELDCNYPDPMVR	612
	. .     ..... .  ::::  :: :: . :::: :: :::	
339	KALTKLLQSTNLREESERVEVLELMDSWAEIDDDALELLGSTFKNLSVR	388
	.....	
613	GFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQY.....	644
	::  .  .   . .  .   :    ::: : ..	
389	SYAVNRLKK.ASDKELELYLLQLVEAVCFENLSTFSDKSNSEFTTIVDAVS	437
	.....	
645	.....LDNLLVRELLKK	656
	: .  .   :::	
438	SQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLPIVISPLAEFLIRR	487



```

657 ALTNQRI G H F F F W H L K S E M H N K I V S O R F G L I L L E S Y . C R A C G M Y L K H L N R Q 705
    | | . | . | : | | | : | . | | | . : : . | . : | . . . | | |
488 ALVNPR L G S F F Y W Y L K S E S E D K P Y . . . L D Q I L S S F W S R L D K K S R N I L N D Q 534
    .
706 V E A M E K L I N L T D I L K Q E K K D E T O K V O M K F . L V E Q M R R P D E M D A L Q G F L S P 754
    | : : | : : . : | . | . . . | : : . | : | . | | : : . : |
535 V R L I N V L R E C C E T I K R L K D T T A K K M E L L V H L L E T K V R P . . L V K V R P I A L P 582
    .
755 I N P A H Q I G N I R L E E C R I M S S A K R P I W L N W E N P D I M S E L L F O N N E I I F K N G 804
    | : | . : : : | : : : : | . . | | : : : . . . | | : : | | |
583 L D P D V L I C D V C P E T S K V F K S S L S P L K I T E K T T . . . . . I N Q P Y H L M F K V G 626
    .
805 D D L R Q D M L T L Q I I R I M E N I W Q N Q G L D L R M L P Y G C L S I G D C V G L I E V V R N S 854
    | | | | | | . : | | | . : : : : | : : : | | : | . | . | . | | | . : |
627 D D L R Q D Q L V V Q I I S I M N E L L K N E N V D L K L T P Y K I L A T G P O E G A T E F I P N . 675
    .
855 H T I M Q I O C K . G G L K G A L Q F N S H T L H Q W L K D K N K G E I Y D A A I D L F T R S C A G 903
    . | : | | : | | : | | . : : : : . : : : : | | . : | | | |
676 D T L A S I L S K Y H G I L G Y L K L . . . . . H Y P D E N A T I G V Q G W L D N F V K S C A G 719
    .
904 Y C V A T F I L G I G D R H S N I M V K D D G Q L F H I D F G H F L D H K K K K F G Y K R E R V P 953
    | | | | : | | | : | | | . | : : | . . | | : : | | | | . |
720 Y C V I T Y I L G V G D R H L D N L L V T P D G H F F H A D F G Y I L G O D P K P F . . . . . P 762
    .
954 F V L T Q D F L I V I S K G A Q E C T K T R E F E R F Q E M C Y K A Y L A I R Q H A N L F I N L F S 1003
    : . . | : . | : | . : : : | . | : | | : | : | . : | | | .
763 P I M K L P P Q I I E A F G G A E S S . . . N Y D K F R S Y C F V A Y S I L R R N A G L I I N L F E 809
    .
1004 M M L G S G M P E . . L Q S F D D I A Y I R K T L A L D K T E Q E A L E Y F M K Q M N D A H H G G W 1051
    : | . | : | : : . : | : | . : | : : | : | . | . : | | . : : :
810 I M K T S N I P D I R I D P N G A I L R V R E R F N L M S E E D A T V H F Q N L I N D S V N A L L 859
    .
1052 T T K M D W I F H T I K Q H 1065
    . . : | : | : | .
860 P I V I D H . L H N L A O Y 872

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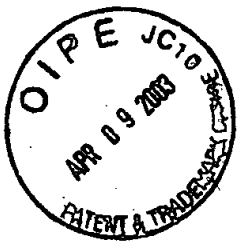


FIG. 11A

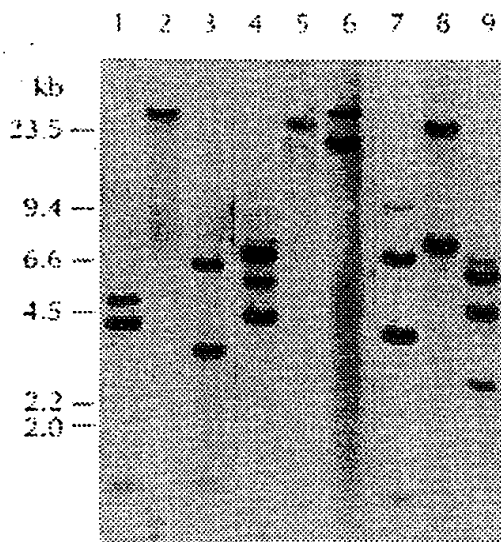
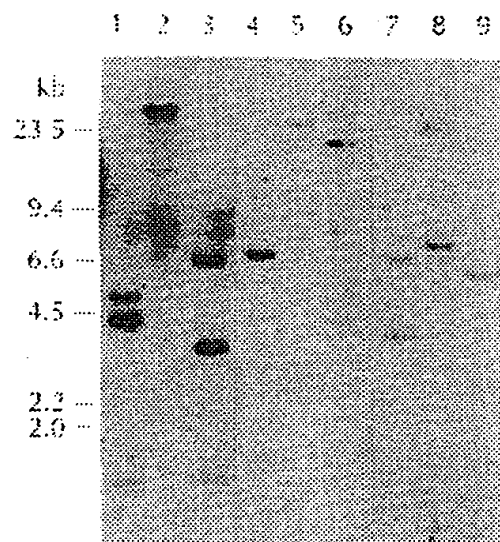


FIG. 11B







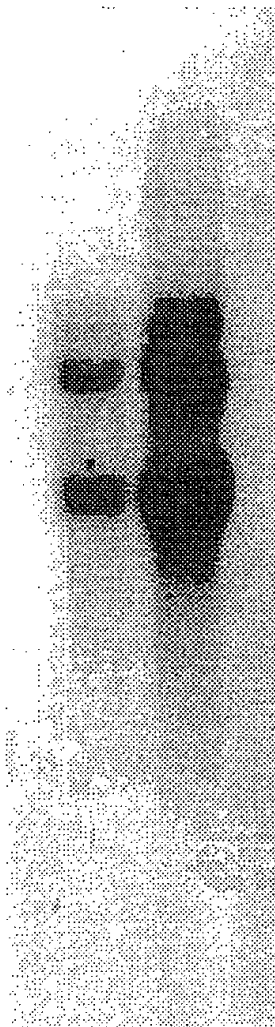
RECEIVED  
APR 09 2003

FIG. 12A

1 2

285 —

185 —



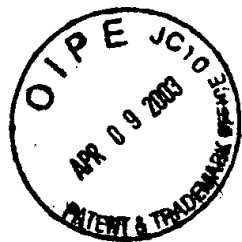


FIG. 12B

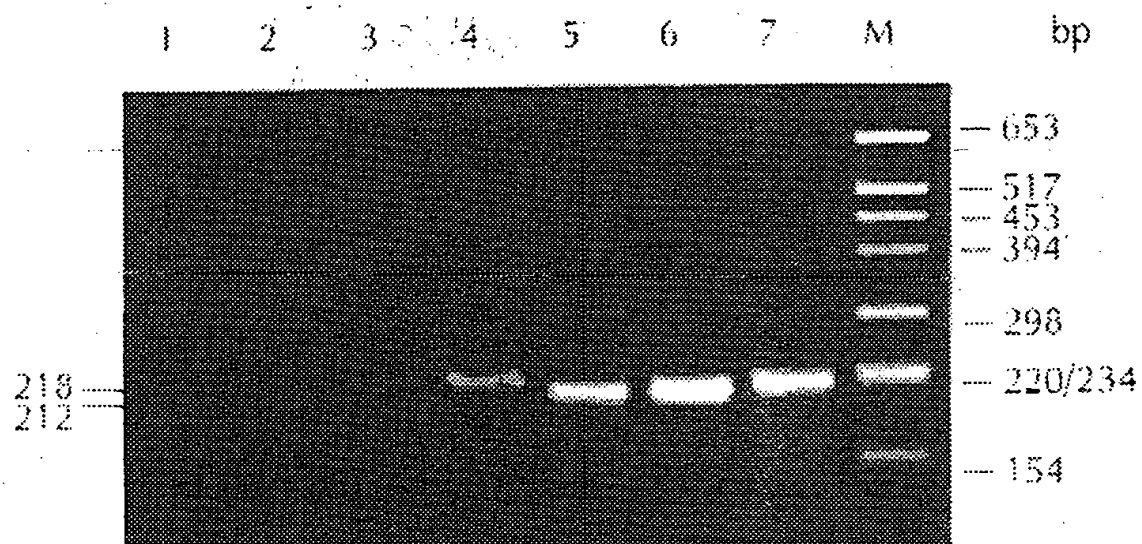


FIG. 12C

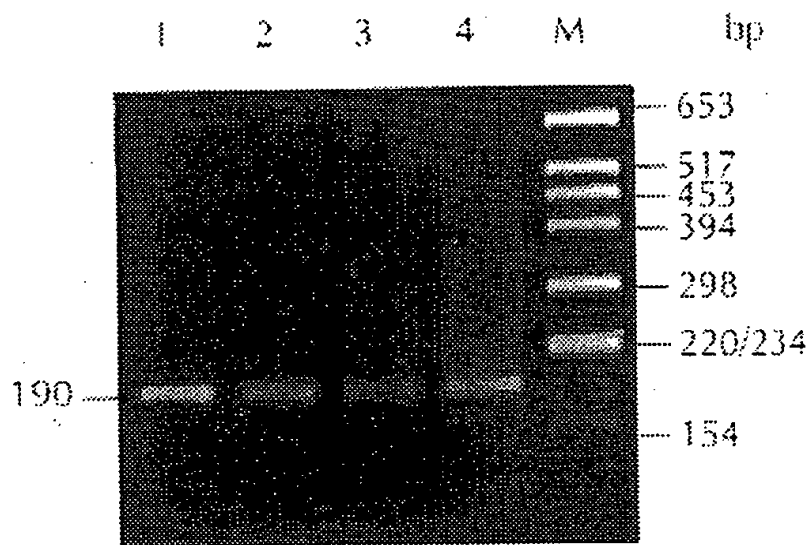




FIG. 13A

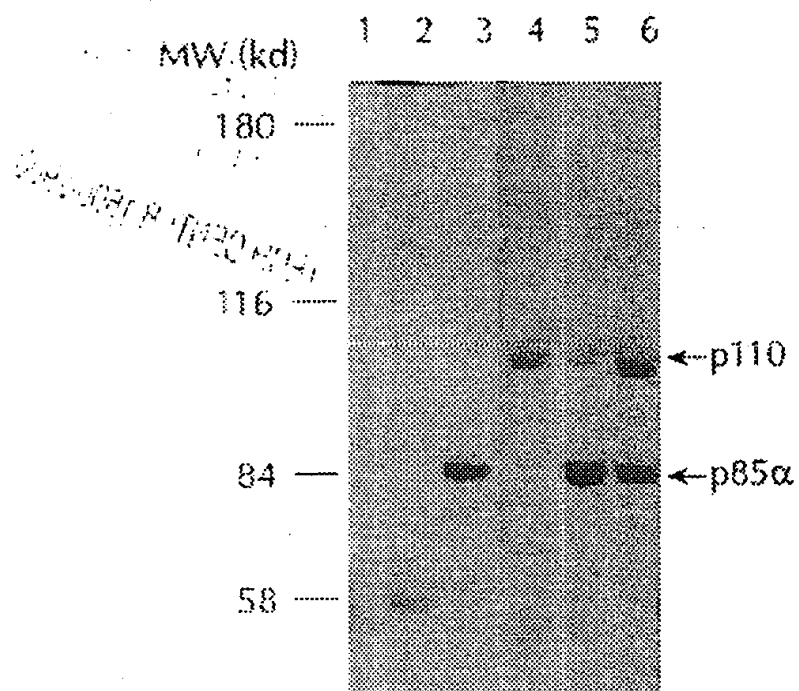
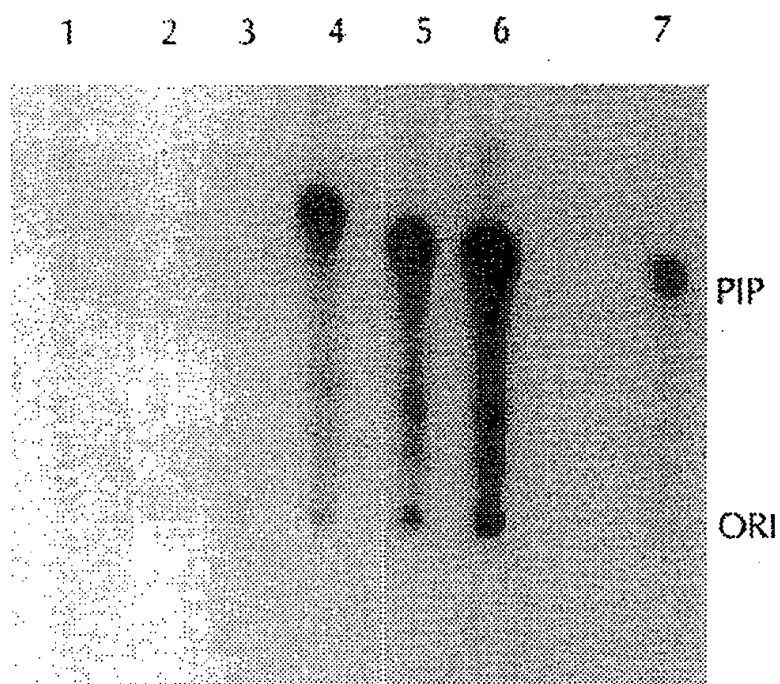


FIG. 13B



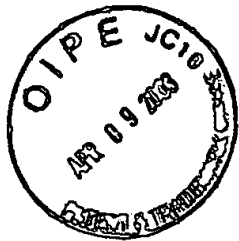


FIG. 14A

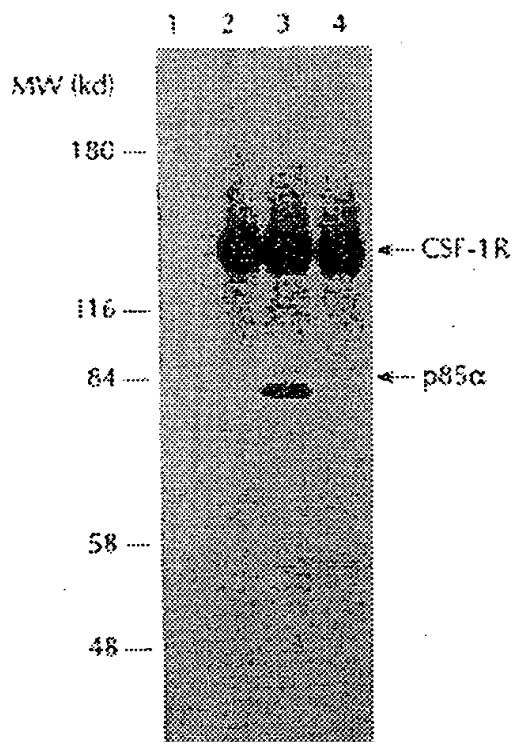


FIG. 14B

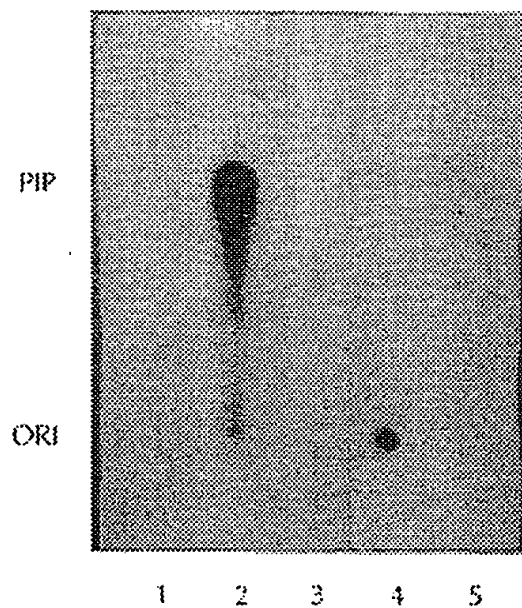


FIG. 15A

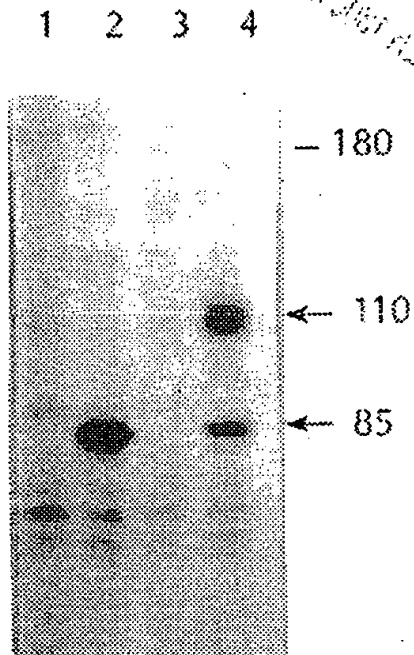


FIG. 15B

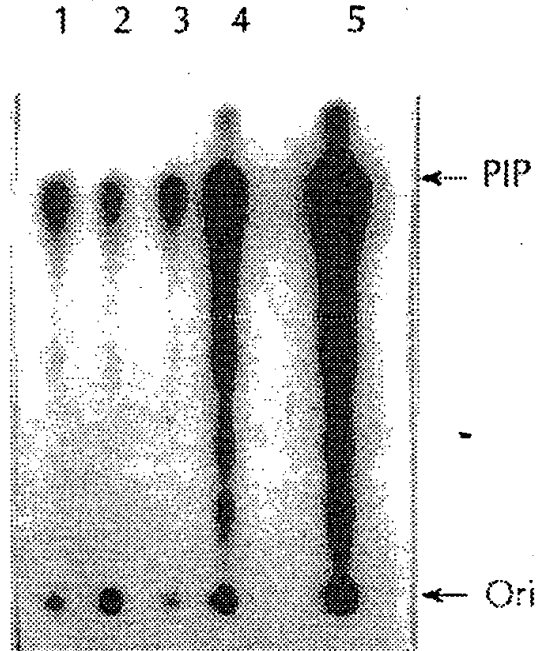


FIG. 15C

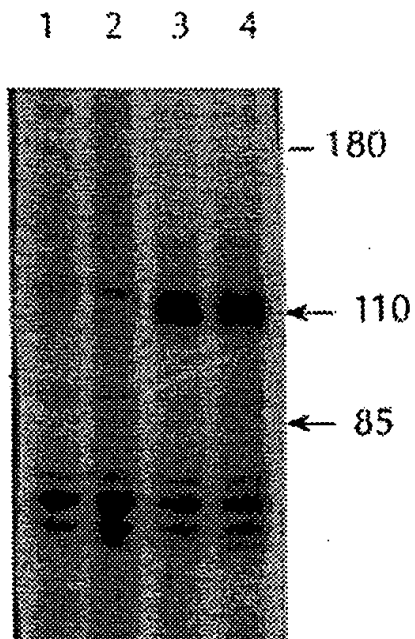
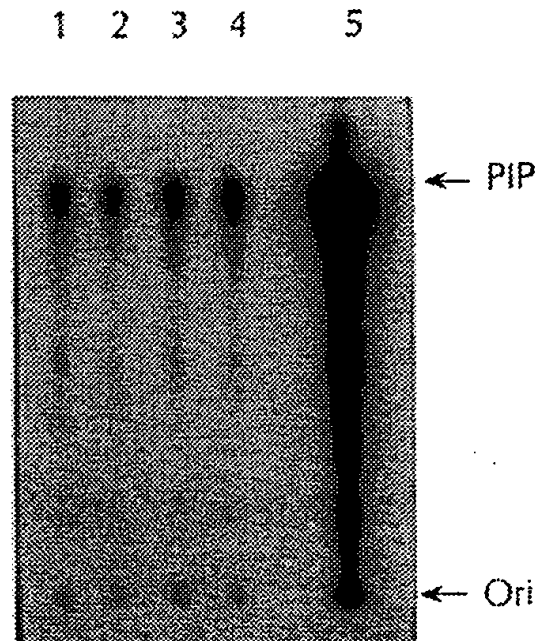
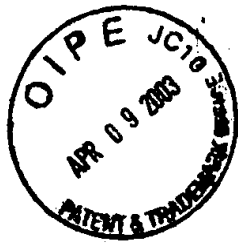


FIG. 15D







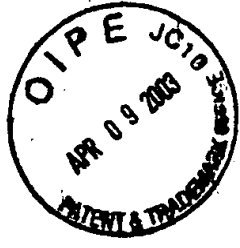
# FIG. 16B

193 GAATCTTTACATTTTCGTAAGTGTTACCCAAAGAACGAGAAAGGGAA  
-----+-----+-----+-----+-----+-----+  
CTTAGAAGAAATGTAAAGCATTCACAATGGGTTCTTCGTCTTTCCCTT  
E S S Y I F V S V T Q E A E R E 240

241 GAATTTTGTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA  
-----+-----+-----+-----+-----+-----+  
CTTAAAAACTACTTTGTTCTGCTGAAACACTAGAACCCGAAAGTT  
E F F D E T R R L C D L R L F Q 288

289 CCATTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATC  
-----+-----+-----+-----+-----+-----+  
GGTAAAAATTTTCATTAACCTTGGTCATCCGTTGGCACTTCTTTCTAG  
P F L K V I E P V G N R E E K I 336

337 CTCAATCGAGAAATTGGTTTGTCTATCGGCATGCCAGTGTGCGAATTT  
-----+-----+-----+-----+-----+-----+  
GAGTTAGCTCTTTAAACCAAAACGATAGCCGTACGGTCACACGCTTAAA  
L N R E I G F A I G M P V C E F 384



## FIG. 16C

385 GATATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGAAATATTCTT 432  
-----+-----+-----+-----+-----+-----+-----  
CTATACCAATTCTAGGACTTCAATGTCCTGAAGGCTTCTTTATAAGAA  
D M V K D P E V Q D F R R N I L

433 AATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480  
-----+-----+-----+-----+-----+-----+-----  
TTACAAACATTTCTTCGACACCTAGAATCCCTAGAATTAAGTGGAGTA  
N V C K E A V D L R D L N S P H

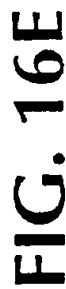
481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 528  
-----+-----+-----+-----+-----+-----+-----  
TCATCTCGTTACATACAGATAGCGGTGTACATCTTAGAAGTGGTCTC  
S R A M Y V Y P P H V E S S P E

529 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTG 576  
-----+-----+-----+-----+-----+-----+-----  
GACGGTTTCGGTGATATATTTAACCTATCTCCGGTTTATATATCAC  
L P K H I Y N K L D R G Q I I V

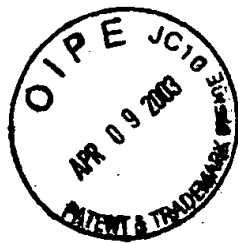




768



769	TGTGATGAATACTTCCTAGAAAAAATATCCTCTGAGTCAGTATAAGTAT -+-----++-----+-----+-----+-----+ ACACTACTTATGAAGGATCTTTTATAGGAGACTCAGTCATATTCATA C D E Y F L E K Y P L S Q Y K Y	816
817	ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTIGAAGATGATG ---+-----+-----+-----+-----+-----+ TATTCTTCGACATATTACGAACCCCTCCTACGGGTTAAACTTCTACTAC I R S C I M L G R M P N L K M M	864
865	GCTAAAGAAAGCCCTTTATTCTCAACTGCCAATGGACTGTTTTACAATG ---+-----+-----+-----+-----+-----+ CGATTTCTTTCGGAAATAAGAGTTGACGGTTACCTGCACAAAATGTTAC A K E S L Y S Q L P M D C F T M	912
913	CCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA ---+-----+-----+-----+-----+-----+ GGTAGAAATAAGGTCTCGGTAAAGGTGTCGATGTGGTATATACTTACCT P S Y S R R I S T A T P Y M N G	960



## FIG. 16F

961	GAAACATCTACAAAATCCCTTTGGGTTATATAATAGAGCACTCAGAATA -----+-----+-----+-----+-----+----- CTTTGTAGATGTTTAGGAAACCCAATATTATCTCGTGAGTCTTAT E T S T K S L W V I N R A L R I	1008
1009	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC -+-----+-----+-----+-----+-----+----- TTTAAAGAAACACGTTGGATGCACCTTAGATTATATAAGCTCTGTAACTG K I L C A T Y V N L N I R D I D	1056
1057	AAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT -----+-----+-----+-----+-----+----- TTCTAAATACAAGCTTGTCCATAGATGGTACCTCCTCTTGGGAATACA K I Y V R T G I Y H G G E P L C	1104
1105	GACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT -----+-----+-----+-----+-----+----- CTGTTACACTTGTGAGTTTCTCATGGAACAAGGTTAGGTTCCACCTTA D N V N T Q R V P C S N P R W N	1152



## FIG. 16G

1153 GAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGTGCTGCT  
-----+-----+-----+-----+-----+-----+  
CTTACCGACTTAATACTATATATGTAAGGACTAGAAAGGACGACGACGA  
E W L N Y D I Y I P D L P R A A 1200

1201 CGACTTTGCCCTTCCATTGTGCTCTGTAAAGGCCGAAAGGGTGCTAAA  
-----+-----+-----+-----+-----+-----+  
GCTGAAACGGAAAGGTAAACGAGACAATTTCCGGCTTTCCCGACGATTT  
R L C L S I C S V K G R K G A K 1248

1249 GAGGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGATTAC  
-+-----+-----+-----+-----+-----+-----+  
CTCCTTGTGACAGGTAACCGTACCCCTTTATATATTGAACAACTAATG  
E E H C P L A W G N I N L F D Y 1296

1297 ACAGACACTCTAGTATCTGAAATAATGGCTTTGAATCTTTGGCCAGTA  
---+-----+-----+-----+-----+-----+-----+  
TGTCTGTGAGATCATAGACCTTTTACCGAACTTAGAAACCGGTCAT  
T D T L V S G K M A L N' L W P V 1344



## FIG. 16H

1345 CCTCATGGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA 1392  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GGAGTACCTAATCTTCTAAACGACTTGGGATAACCAACAATGACCTAGT  
P H G L E D L L N P I G V T G S

1393 AATCCAAATAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC 1440  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TTAGGTTTATTCTTTGAGGTACGAATCTCAACCTCAAACCTGACCAAG  
N P N K E T P C L E L E F D W F

1441 AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1488  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TCGTCACACCATTTCAAGGGTCTATACAGTCACCTAACTTCTCGTACGG  
S S V V K F P D M S V I E E H A

1489 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGA 1536  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TTAACCAACACATAGGGCTCTTCGTCCTAAATCGATAAGGTGCGTCCT  
N W S V S R E A G F S Y S H A G

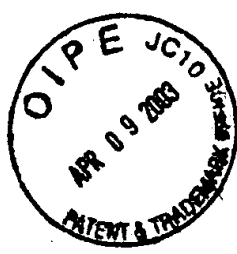
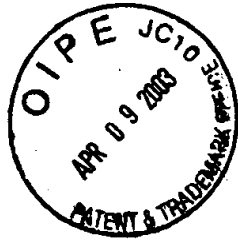


FIG. 161

1537	CTGAGTAACAGACTAGCTAGAGACAAATGAATTAAGGGAATAATGACAAA -----+-----+-----+-----+-----+----- GACTCATTTGCTGATCGATCTCTGTTACTTAATTCCTTTTACTGTTT L S N R L A R D N E L R E N D K	1584
1585	GAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACT -----+-----+-----+-----+-----+----- CTTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGAGACTTTAGTGA E Q L K A I S T R D P L S E I T	1632
1633	GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC -----+-----+-----+-----+-----+----- CTCGTCCCTCTTTCTAAAGATAACCTCAGTGTCTGTGATAACACATTGA E Q E K D F L W S H R H Y C V T	1680
1681	ATCCCCGAAATTCTACCCCAAATTGCTTCTGTCTGTTAAATGGAATTCT -----+-----+-----+-----+-----+----- TAGGGGCTTTAAGATGGGTTTAAACGAAGACAGACAATTTACCTTAAGA I P E I L P K L L L S V K W N S	1728



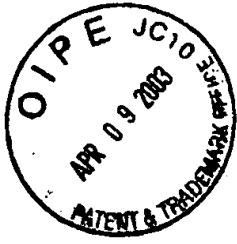
## FIG. 16J

1729 AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCA 1776  
-+-----+-----+-----+-----+-----+-----+-----+-----+  
TCTCTACTTCATCGGGTCTACATAACGAACCATTTTCTAACCGGAGGT  
R D E V A Q M Y C L V K D W P P

1777 ATCAAACCTGAACAGGCTATGGAACCTTCTGGACTGTAATTACCCAGAT 1824  
-+-----+-----+-----+-----+-----+-----+-----+-----+  
TAGTTTGACTTGTCGGATACCTTGAAGACCCTGACATTAATGGGTCTA  
I K P E Q A M E L L D C N Y P D

1825 CCTATGGTTCGAGGTTTGTGCTGTTCCGGTCTTGGAAAAATATTTAACA 1872  
-+-----+-----+-----+-----+-----+-----+-----+-----+  
GGATACCAAGCTCCAAAACGACAAGCCACGAAACCTTTTATATAAATTGT  
P M V R G F A V R C L E K Y L T

1873 GATGACAAACTTCTCAGTATTTAATTTCAGCTAGTACAGGTCCTAAAA 1920  
-+-----+-----+-----+-----+-----+-----+-----+-----+  
CTACTGTTTGAAAGAGTCATAAATTAAAGTCGATCATGTCCAGGATTTT  
D D K L S Q Y L L I Q L V Q V L K



## FIG. 16K

1921 TATGAACAATATTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA  
-----+-----+-----+-----+-----+-----  
1968 ATACTTGTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT  
Y E Q Y L D N L L V R F L L K K  
1969 GCATTGACTAATCAAAGGATTGGCACTTTTCTTTTGGCATTTAAAA  
-----+-----+-----+-----+-----+-----  
2016 CGTAACTGATTAGTTTCCTAACCCGTGAAAAAGAAAAACCGTAAATTT  
A L T N Q R I G H F F F W H L K  
2017 TCTGAGATGCACAATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTG  
-----+-----+-----+-----+-----+-----  
2064 AGACTCTACGTGTTATTTGTCAATCGGTCTCCAAACCGGACGAAAC  
S E M H N K T V S Q R F G L L L  
2065 GAGTCCTATTGTCGTCATGTGGGATGTATTTGAAGCACCTGAATAGG  
-----+-----+-----+-----+-----+-----  
2112 CTCAGGATAACAGCACGTACACCCCTACATAAACTTCGTGGACTTATCC  
E S Y C R A C G M Y L K ' H L N R





## FIG. 16L

2113	CAAGTCGAGGCAATGGAAGCTCATTAACCTAACTGACATTTCTCAAA -----+-----+-----+-----+-----+-----+-----+ GTTCAGCTCCGTTACCTTTTCGAGTAATTGAATTGACTGTAAGAGTTT Q V E A M E K L I N L T D I L K	2160
2161	CAGGAGAGGAAGGATGAACACAAAGGTACAGATGAAGTTTTAGTT -----+-----+-----+-----+-----+-----+-----+ GTCCTCTCCTTCCCTACTTTGTGTTTTCATGTCTACTTCAAAAATCAA Q E R K D E T Q K V Q M K F L V	2208
2209	GAGCAAATGAGCGCACCAGATTTTCATGGATGCCCTACAGGGCTTGCTG -+-----+-----+-----+-----+-----+-----+ CTCGTTTACTCCGCTGGTCTAAAGTACCTACGGGATGTCCCGAAGGAC E Q M R R P D F M D A L Q G L L	2256
2257	TCTCCTCTAAACCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAG ---+-----+-----+-----+-----+-----+-----+ AGAGGAGATTTGGACGAGTAGTTGATCCCTTTGGAGTCCGAATTCTC S P L N P A H Q L G N L 'R L K E	2304



**FIG. 16M**

[illegible]



2497	ATGTTACCTTATGGTTGCTCTGTCAATCGGTGACTGTGTGGGACTTATT ---+---+---+---+---+---+---+---+---+---+---+---+ TACAATGGAATACCAACAGACAGTTAGCCACTGACACACCCCTGAATAA M L P Y G C L S I G D C V G L I	2544
2545	GAGGTGGTCCGAAATTCTCACACTATTATGCAAAATTCAGTGCAAAGGC ---+---+---+---+---+---+---+---+---+---+---+---+ CTCACCCACGCTTTAAGAGGTGATAATAACGTTTAAGTCACGTTTCCG E V V R N S H T I M Q I Q C K G	2592
2593	GGCTTGAAAGGTGCACCTGCAGTTCAACAGCCACACACTACATCAGTGG ---+---+---+---+---+---+---+---+---+---+---+---+ CCGAACTTTCACCGTGACGTCAAGTTGTCGGTGTGTGATGTAGTCACC G L K G A L Q F N S H T L H Q W	2640
2641	CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG ---+---+---+---+---+---+---+---+---+---+---+---+ GAGTTTCTGTCTGTTCCTCTTATATACTACGTGCGTAACTGGAC L K D K N K G E I Y D A A I D L	2688



# FIG. 160

2689	TTTACCGTTCA	TGCTGGATACTGT	GTAGCTACCTTC	ATTCTTGGGA	2736
	-+-----+	-----+	-----+	-----+	
	AAATGTGCAAG	TACACGACCTATG	ACACATCGATG	GAAAGTAAACCC	
	F T R S C A	G Y C V A T	F I L G		
2737	ATTGGAGATCG	TCAATAAGTAACA	TATCATGGTGAA	GACGATGGACAA	2784
	-----+	-----+	-----+	-----+	
	TAACCTCTAGC	AGTGTATCATTTG	TAGTACCACCTT	TCTGCTACCTG	
	I G D R H N	S N I M V K	D D G Q		
2785	CTGTTTCATA	TATGATTTTGGAC	ACTTTTGGATCA	CAAGAAAGAAAA	2832
	-----+	-----+	-----+	-----+	
	GACAAAGTATA	CTAAACCTGTGAA	AAACCTAGTGT	CTCTTTT	
	L F H I D F	G H F L D H	K K K K		
2833	TTTGGTTATA	AACGAGAACGTGT	GCCATTGTTT	TGACACAGGATTC	2880
	-----+	-----+	-----+	-----+	
	AAACCAATA	TTTGCTTTCACAC	GCGTAAACAAA	AACTGTCTCTAA	
	F G Y K R E	R V P F V L	T Q D F		



## FIG. 16P

2881	TTAATAGTGATTAGTAAAGGAGCCCAAGAAATGCACAAAGACAAGAGAA -----+-----+-----+-----+-----+----- AATTACACTAATCATTTCCCTCGGGTTCTTACGTGTTTCTGTCTCTT L I V I S K G A Q E C T K T R E	2928
2929	TTTGAGAGGTTTCAGGAGATGTGTACAAAGGCTTATCTAGCTATTCCA -----+-----+-----+-----+-----+----- AAACTCTCCAAGTCCCTCTACACAAATGTTCCGAATAGATCGATAAGCT F E R F Q E M C Y K A Y L A I R	2976
2977	CAGCATGCCAATCTCTCATAAATCTTTTCTCAATGATGCTTGGCTCT -----+-----+-----+-----+-----+----- GTCGTACGGTTAGAGAAAGTATTTAGAAAGAGTTACTACGAACCGAGA Q H A N L F I N L F S M M L G S	3024
3025	GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG -----+-----+-----+-----+-----+----- CCTTACGGTCTTGATGTTAGAAAACACTACTGTAACGTATGTAAGCTTTC G M P E L Q S F D D I A Y I R K	3072

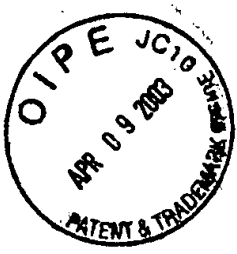


FIG. 16Q

3073	ACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTCATG -----+-----+-----+-----+-----+-----+ TGGGATCGGAATCTATTTTGACTCGTTCTCCGAAACCTCATAAAGTAC T L A L D K T E Q E A L E Y F M	3120
3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT -----+-----+-----+-----+-----+-----+ TTTGTTTACTTACTACGTGTAGTACCACCGACCTGTTGTTTACCTA K Q M N D A H H G G W T T K M D	3168
3169	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACT -+-----+-----+-----+-----+-----+-----+ ACCTAGAAGGTGTGTTAATTGTGCGTACGTAACCTTGACTTCTCTATTGA W I F H T I K Q H A L N *	3216
3217	GAGAAAATGAAAGCTCACTCTGGATTCCACACTGCACCTGTTAATAACT -+-----+-----+-----+-----+-----+-----+ CTCTTTTACTTTCGAGTGAGACCCTAAGGTGTGACGTGACAATTATTGA	3264



3265 CTCAGCAGGCAAGACCGATTGCATAGGAATTGCACCAATCCATGAACA  
 ---+-----+-----+-----+-----+-----+-----+  
 3312 GAGTCGTCGGTTCTGGCTAACGTATCCTTAACGTGTTAGGTACTTGT

3313 GCATTAGATTACAGCAAGAACAGAAATAAAATACTATATAATTAAA  
-----+-----+-----+-----+-----+-----+  
3360 CGTAATCTAAATGTCGTTCTTGTCTTTATTTATGATATATAATAATT

3361  
TAAATGTAACGCACAAACAGGGTTTGATAGCACTTAACCTAGTTCATTC  
-----+-----+-----+-----+-----  
ATTACATTTGCGTTTGTCCTCCAAACTATCGTGAAATTGATCAAGTAAAG  
3408

AAAA	3409
-+--	3412
TTTT	



## FIG. 17A

hum110 1 ATGCCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50  
|||||  
bov110 1 ATGCCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50  
|||||

51 CCCAAGAATCCTAGTGGAATGTTACTACCAAAATGGAATGATAGTGACTT 100  
|||||

51 CCCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGGATGATAGTGACTT 100  
|||||

101 TAGAATGCCCTCCGTGAGGCTACATTAGTAACCTATAAAGCATGAACCTATTT 150  
|||||

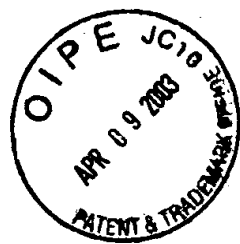
101 TAGAATGCCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACCTATTT 150  
|||||

151 AAAGAAGCAAGAAATAACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200  
|||||

151 AAAGAAGCAAGAAATAACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200  
|||||







## FIG. 17C

451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGCAATGTATGTCTA 500  
|||||  
451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGCAATGTATGTTTA 500  
|||||  
501 TCCGCCACATGTAGAAATCTTCCACAGAGCTGCCAAAGCACATATAATA 550  
|||||  
501 TCCTCCAAATGTAGAAATCTTCCACAGAACTGCCAAAGCACATATAATA 550  
|||||  
551 AATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTAATAGTTTCTCCA 600  
|||||  
551 AATTGGATAAAGGGCAAATAATAGTGGTGATTGGGTAATAGTTTCTCCA 600  
|||||  
601 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650  
|||||  
601 AATAATGACAACACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650  
|||||  
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGC 700  
|||||  
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGC 700



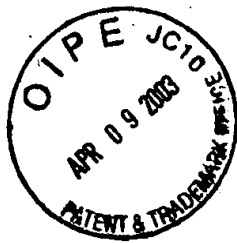
## FIG. 17D

701 TATCATCTGAACAATTAAAACTCTGTGTTTGAATATCAGGCAAGTAC 750  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
701 TATCATCTGAACAACAATAAACTCTGTGTTTGAATATCAGGCAAGTAT 750  
751 ATTTTAAAGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT 800  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
751 ATTTTAAAGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT 800  
801 GAGTCAGTATAAGTATAAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
801 GAGTCAGTATAAGTATAAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850  
851 ATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 900  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
851 ATTTGATGCTGATGGCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGAC 900  
901 TGTTTTACAATGCCCATCTTATTCCAGACGCATTTCCACAGCTACACCATA 950  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
901 TGTTTTACAATGCCCATCATATTCCAGACGCATCTCCACAGCTACGCCATA 950



## FIG. 17E

951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC 1000  
|||||  
951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCAC 1000  
|||||  
1001 TCAGAAATAAAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC 1050  
|||||  
1001 TCAGAAATAAAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC 1050  
|||||  
1051 ATTGACAAGATTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100  
|||||  
1051 ATTGACAAGATTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100  
|||||  
1101 ATGTGACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150  
|||||  
1101 ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150  
|||||  
1151 ATGAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200  
|||||  
1151 ATGAATGGCTGAATTACGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200  
|||||

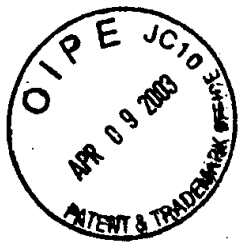


## FIG. 17F

1201 CGACTTTGCCCTTTCCATTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250  
|||||  
1201 CGACTTTGCCCTTTCCATTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250  
1251 GGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGATTACACAG 1300  
|||||  
1251 GGAACACTGTCCATTGGCCCTGGGGAATAATAAACTTGTGATTACACAG 1300  
1301 AACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350  
|||||  
1301 AACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350  
1351 GGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400  
|||  
1351 GGACTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400  
1401 TAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450  
|||||  
1401 TAAAGAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450



1451	TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
1451	TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
1501	TCCCGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACT	1550
1501	TCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTGAGTAACAGACT	1550
1551	AGCTAGAGACAAATGAATTAAGGGAAATGACAAAGAACAGCTCAAAGCAA	1600
1551	AGCTAGAGACAAATGAATTAAGAGAAATGATAAGAACAGCTCCGAGCAA	1600
1601	TTTCTACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTT	1650
1601	TTTGTACACGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAGATTTT	1650
1651	CTATGGAGTCACAGACACTATTGTGTAACATATCCCCGAAATTCTACCCAA	1700
1651	CTGTGAGCCACAGACACTATTGTGTAACATATCCCCGAAATTCTACCCAA	1700



## FIG. 17H

1701 ATTGCTTCTGCTGTTAAATGGAAATTCAGAGATGAAGTAGCCAGATGT 1750  
|||||  
1701 ATTGCTTCTGCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750  
|||||  
1751 ATTGCTTGGTAAAGATTGGCCCTCCAATCAAACCTGAACAGGCTATGGAA 1800  
|||||  
1751 ACTGCTTGGTAAAGATTGGCCCTCCAATCAAGCCTGAACAGGCTATGGAG 1800  
|||||  
1801 CTTCTGGACTGTAAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCCG 1850  
|||||  
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCCG 1850  
|||||  
1851 GTGCTTGGAAAAATATTAAACAGATGACAAACTTCTCAGTATTTAATTC 1900  
|||||  
1851 GTGCTTAGAAAAATATTAAACAGATGACAAACTTCTCAGTACCCTAATTC 1900  
|||||  
1901 AGCTAGTACAGGTCCTAAAAATATGAACAATATTGGATAACTTGCTTGTTG 1950  
|||||  
1901 AGCTAGTACAGGTACTAAAAATATGAACAGTATTGGATAACCTGCTTGTTG 1950

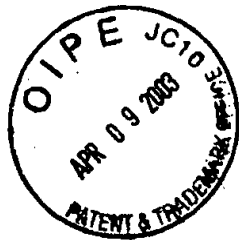






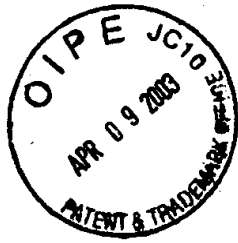
FIG. 17J

2201 TTTAGTTGAGCAAAATGAGGCGACAGATTTCATGGATGCCCTACAGGGC 2250  
|||||  
2201 TTTAGTTGAGCAAAATGCGGCGACAGATTTCATGGATGCTCTCCAGGGC 2250  
|||||  
2251 TTGCTGTCTCCTCTAAACCCCTGCTCATCACTAGGAAACCTCAGGCTTAA 2300  
||  
2251 TTTCTGTCTCCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300  
|||||  
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350  
|||||  
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350  
|||||  
2351 AGAACCAGACATCATGTCTCAGAGTTACTGTTCAGAAACAATGAGATCATC 2400  
|||||  
2351 AGAACCAGACATCATGTCTCAGAAATTACTCTTTCAGAAACAATGAGATCATC 2400  
|||||  
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAATTAT 2450  
|||||  
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACCCCTTCAGATTAT 2450



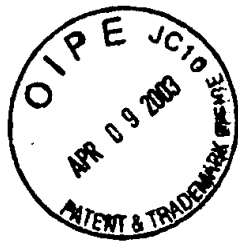
**FIG. 17K**

2451	TCGTATTATGGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGT	2500
2451	TCGCATTATGGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAATGT	2500
2501	TACCTTATGGTTGTCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTG	2550
2501	TACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGACTTATCGAGGTG	2550
2551	GTGCGAAATTCTCACACTATTATGCAAATTCAGTGCAAAGCGGCTTGAA	2600
2551	GTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAGGAGGCCTGAA	2600
2601	AGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGGCTCAAAGACA	2650
2601	AGGTGCACTGCAGTTTAAACAGCCACACACTCCATCAGTGGCTCAAAGACA	2650
2651	AGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2700
2651	AGAACAAAGGGGAAATATATGATGCGGCCATCGATTGTTTACACGATCA	2700



## FIG. 17L

2701 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA 2750  
|||||  
2701 TGTGCTGGATAATTGTGTGCCACCTTCATTTTGGGAATTGGAGATCGTCA 2750  
|||||  
2751 CAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATT 2800  
|||||  
2751 CAATAGTAATATCATGGTTAAAGATGATGGACAACCTGTTTCATATAGATT 2800  
|||||  
2801 TTGGACACTTTTGGATCACAAGAGAAAAATTGGTTATAAACGAGAA 2850  
|||||  
2801 TTGGACACTTTTGGATCACAAGAGAAAAATTGGTTATAAACGAGAG 2850  
|||||  
2851 CGTGTGCCATTGTGTTTGACACAGGATTCTTAATAGTGATTAGTAAAGG 2900  
|||  
2851 CGCGTGCCGTTGTGTTTGACACACAAGATTCTTAATAGTGATTAGTAAAGG 2900  
|||||  
2901 AGCCCAAGAAATGCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950  
|||||  
2901 AGCCCAAGAAATGCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950



## FIG. 17M

2951 GTTACAAGGCTTATCTAGCTATTGACAGCATGCCAATCTCTCATAAAT 3000  
|||||  
2951 GTTACAAGGCTTATCTAGCTATTGCGCAGCATGCCAATCTCTCATAAAT 3000  
|||||  
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGA 3050  
|||||  
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGA 3050  
|||||  
3051 TGACATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAG 3100  
|||  
3051 TGATATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAACTGAGCAAG 3100  
|||||  
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGC 3150  
|||||  
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACACCATGGTGGC 3150  
|||||  
3151 TGGACAACAAAATGGATTGGATCTTCCACACAATTAACAGCATGCATT 3200  
|||||  
3151 TGGACAACAAAATGGATTGGATCTTCCACACAATTAAGCAGCATGCTTT 3200  
|||||  
3201 GAACTGAAAGATAAAGTGAAGAAATGAAAGCTCACTCTGGA  
|||||  
3201 GAACTGA.....

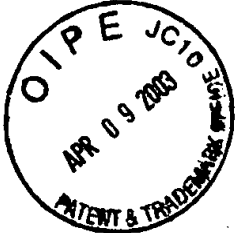


FIG. 18A

10	20	30	40	50	60
h	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ				
b	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ				
10	20	30	40	50	60
70	80	90	100	110	120
h	LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFPQFLKVIIEPVGNREEKILNREIGFA				
b	LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFPQFLKVIIEPVGNREEKILNREIGFA				
70	80	90	100	110	120
130	140	150	160	170	180
h	IGMPVCEFDVKDPQDERRNINLVCKEAVDLRDLNSPHSRAMYVYPHVESSPELPHK				
b	IGMPVCEFDVKDPQDERRNINLVCKEAVDLRDLNSPHSRAMYVYPHVESSPELPHK				
130	140	150	160	170	180

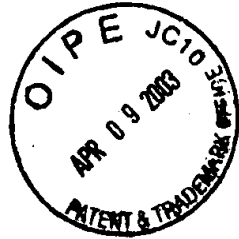
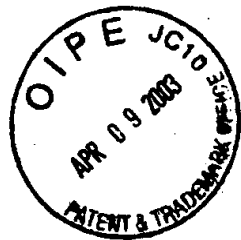


FIG. 18B

190	200	210	220	230	240
h	IYNKLDRGQII	VVIVSPNNDKQKYTLKINHDCVPEQVIAEAI	RKKTRSM	LLSSEQLK	
	:				
b	IYNKLDKGQII	VVIVSPNNDKQKYTLKINHDCVPEQVIAEAI	RKKTRSM	LLSSEQLK	
190	200	210	220	230	240
250	260	270	280	290	300
h	LCVLEYQGYILK	VCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLK	MMAKESLYSQLPMD		
b	LCVLEYQGYILK	VCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLK	MMAKESLYSQLPMD		
250	260	270	280	290	300
310	320	330	340	350	360
h	CFTMPYSRR	ISTATPYMNGETSTKSLWV	INRALRIKILCATYV	NLNIRDIDKIYVRTGI	
b	CFTMPYSRR	ISTATPYMNGETSTKSLWV	INRALRIKILCATYV	NLNIRDIDKIYVRTGI	
310	320	330	340	350	360



## FIG. 18C

370 380 390 400 410 420  
h YHGEPLCDNVNTQRVPCSNPRWNEWLNVDIYIPDLPRARLCLCSVKGRKGAKEEHC  
|||||  
b YHGEPLCDNVNTQRVPCSNPRWNEWLNVDIYIPDLPRARLCLCSVKGRKGAKEEHC  
370 380 390 400 410 420

430 440 450 460 470 480  
h PLAWGNINLFDYTDTLVSGKMAINLWVPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF  
|||||  
b PLAWGNINLFDYTDTLVSGKMAINLWVPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF  
430 440 450 460 470 480

490 500 510 520 530 540  
h SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTRDPL  
|||||  
b SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL  
490 500 510 520 530 540

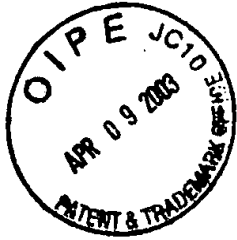


FIG. 18D

550 560 570 580 590 600  
h SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWSRDEVAQMYCLVKDWPPIKPEQAME  
|||||  
b SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWSRDEVAQMYCLVKDWPPIKPEQAME  
550 560 570 580 590 600

610 620 630 640 650 660  
h LLDNCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLKKALTN  
|||||  
b LLDNCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLKKALTN  
610 620 630 640 650 660

670 680 690 700 710 720  
h QRIGHFFFHWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLNLTDLK  
|||||  
b QRIGHFFFHWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLNLTDLK  
670 680 690 700 710 720





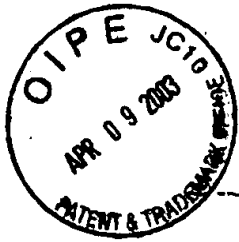
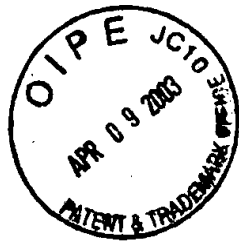


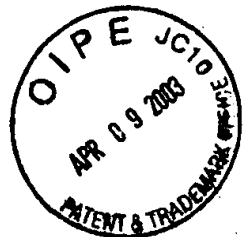
FIG. 18F

910	920	930	940	950	960
h	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF				
b	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF				
910	920	930	940	950	960
970	980	990	1000	1010	1020
h	LIVISKGAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA				
b	LIVISKGAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA				
970	980	990	1000	1010	1020
1030	1040	1050	1060	1070	1080
h	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXKITEKMKAHSG				
b	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNX				
1030	1040	1050	1060		



## FIG. 19A

1 MPPRPSSGEL WGIHLMPPRI LVECLLPNGM IVTLECLREA TLVTIKHELF  
51 KEARKYPLHQ LLQDESSYIF VSVTQEAERE EEFDETRRLC DLRLFQPFLLK  
101 VIEPVGNREE KIILNREIGFA IGMPVCEFDN VKDPEVQDER RNILNVCKEA  
151 VDLRDINSPH SRAMYVYPPH VESSPELPKH IYNKLDRGQI IVVIWVIVSP  
201 NNDKQKYTLK INHDCVPEQV IAEAIRKKTR SMLLSSEQLK LCVLEYQGGY  
251 ILKVCGCDEY FLEKYPLSQY KYIRSCIMLG RMPNLKMMAK ESLYSQLPMD  
301 CFTMPYSRR ISTATPYMNG ETSTKSLWVI NRALRIKILC ATYVNLNIRD  
351 IDKIYVRTGI YHGGEPLCDN VNTQVRPCSN PRWNEWLNVD IYIPDLPRAA  
401 RLCLSICSVK GRKGAKKEHC PLAWGNINLF DYTDTLVSGK MALNLWVPH  
451 GLEDLNPIG VTGSNPNKET PCLELEFDWF SSVVKFPDMS VIEEHANWSV



## FIG. 19B

501 SREAGESYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF  
551 LWSHRHYCVT IPEILPKLL SVKWSRDEV AQMYCLVKDW PPIKPEQAME  
601 LLDCNYPDPM VRGFAVRCLE KYLTDDKLSQ YLIQLVQVLK YEQYLDNLLV  
651 RELKKALTN QRIGHEFFWH LKSEMHNKTV SQRFGLLES YCRACGMYLK  
701 HLNROVEAME KLINLTDILK QERKDETQKV QMKFLVEQMR RPDFMDALQG  
751 LLSPLNPAHQ LGNLRKECR IMSSAKRPLW LNWENPDIMS ELLFQNNNEII  
801 FKNGDDLQRD MLTLQIIRIM ENIWQNQGLD LRMLPYGCLS IGDCVGLIEV  
851 VRNSHTIMQI QCKGGLKGAL QFNSHTLHQW LKDKNKGEIY DAAIDLETRS  
901 CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHFLDH KKKKFGYKRE  
951 RVFVLTQDF LIVISKGAQE CTKTREFFERF QEMCYKAYLA IRQHANLFIN  
1001 LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM QOMNDAHGG  
1051 WTTKMDWIFH TIKQHALN\*

## FIG. 20

1 GGAGACGACTTGGACAGGATCAACTTATCTTCAAAATCATTTCACTC  
GlyAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu

49 ATGGACAAGCTGTACGGAAGAAATCTGGACTTGAAATTGACACCT  
MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro

97 TATAAGGTGTAGCCACCAGTACAAACATGGCTTCATGCAGTTATC  
TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle

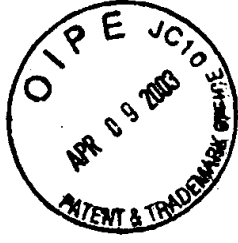
145 CAGTCAGTtCCTGTGGCTGAaGTTCTTGATACAGAGGAAGCATTCAG  
GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln

193 AACTTTTTTAGAAAATATGCACCAGTGAGAAATGGCCAAATGGGATT  
AsnPhePheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle

241 AGTGCTGAGGTCA TGACACTtACGTTAAAGCTGTGCTGGATATGC  
SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys

289 GTGATCACCTATATACTTGGAGTTGGAGACAGCACCTGGATAACCTT  
ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu

337 TTGCTAACCAAAACAGGCAAACTCTTCCACATCGATTTCGGCCAC  
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis



## FIG. 21

1 GGGATGACTTACGGCAGGACATGCTAACGGTCAGATGATTCGCATC  
GlyAspAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

49 ATGAGCAAGATCTGGTCCAGAGGGGCTGGACATGCGCATGGTCATC  
MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

97 TTCCGCTGCTTCTCCACCGCGCGGCGAGAGGGATGGTGGAGATGATC  
PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145 CCTAATGCTGAGACCCCTGCGTAAGATCCAGGTGAGCATGGGTGACC  
ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193 GGCTCGTTCAAGGACCGGCCCTGGCAGACCGGCTGCAGAAACACAAC  
GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241 CCTGGGAGGACGAGTATGAGAAGGCTGTGGaGAACCTTATCTACTCC  
ProGlyGluAspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289 TGGCTGGCTGCTGCGTGGCCACGTACGTCTTGGGCATCTGTGACCga  
CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg

337 CATAATGACAACATCATGCTGAAGACCACCTGGTCACATGTTCCACATC  
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC  
AspPheGly

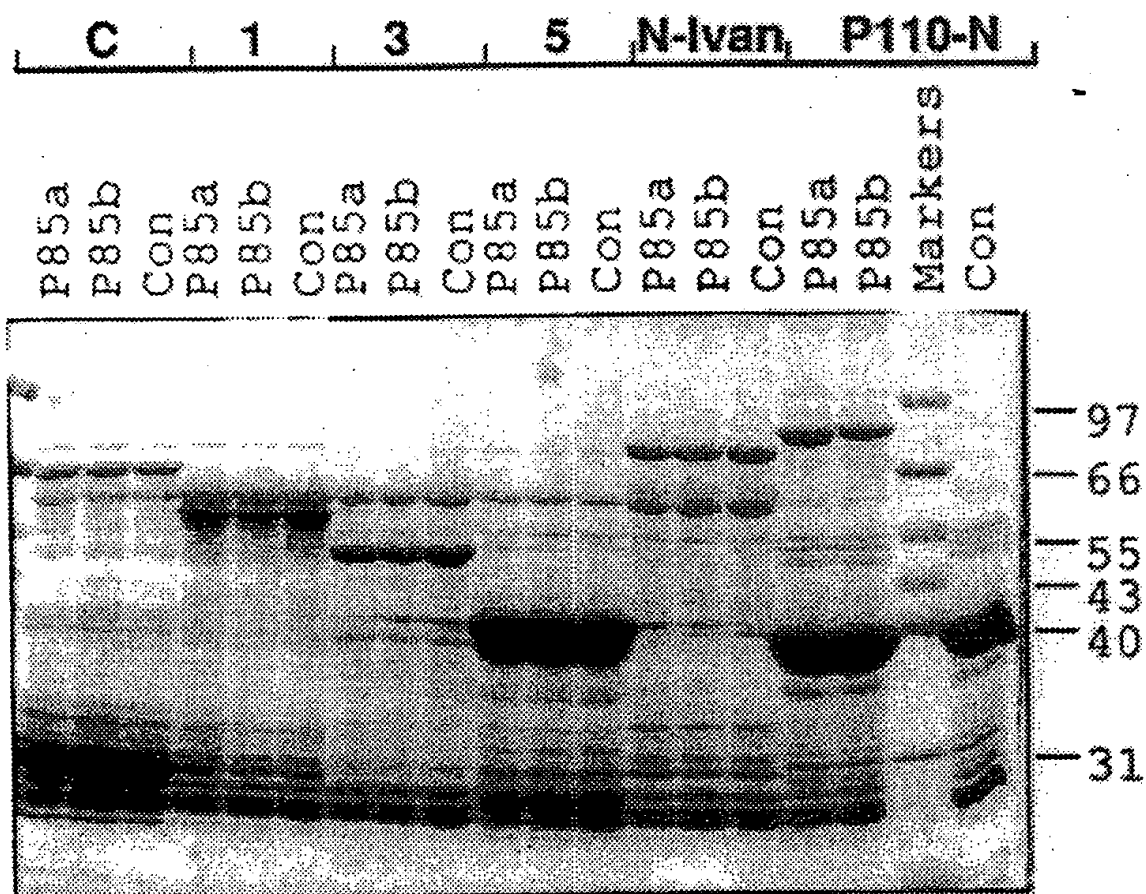
## FIG. 22

1 50  
vps34 GDDLRRQDqLvVQIIslMnellknEnvDLkLtPYkiLaTGpqeGaIEfIPN  
PITR-c GDDLRRQDqLiLQIIslMdkllrkenLDLkLtPYkylLaTstkhGfmqfiqs  
hump110 GDDLRRQDmLtLQIIriMeniwqnqgDLrMlPYgclsiGdcvGLIEvVrN  
PITR-f GDDLRRQDmLtLQmIriMskiwwqEgLDmMrMviFrcFSTGrGrGMVEmIPN  
Consensus GDDLRRQD-L-LQII--M-----E-LDL---PY--L-TG---G-IE-I-N

51 100  
vps34 dtlasilskyhGIlgY.....LklhypdenatlgVqgwvlDnFvkSCA  
PITR-c vpvaevldegsIqnf.....FrkYapsenGpngIsaevmDtYVksCA  
hump110 shtimqiqckgGlkGalqfnshLtLhqWlkdNkge.IydaaiDLftrSCA  
PITR-f aetlrkiqvehGvtGs..fkdrpLadrIqkhNpgedeyekavEnFIySCA  
Consensus -----GI-G-----L-----N-----I-----D-FV-SCA

101 133  
vps34 GYCViTYILGVGDRHLDNllvtpdGhFFHaDEG  
PITR-c GYCViTYILGVGDRHLDNlltktGkLFHIDEF  
hump110 GYCVaTFILGIGDRHnsNiMvkddGqLFHIDEF  
PITR-f GCCVaTYVLGICDRHnDNiMlktGhMFHIDEF  
Consensus GYCV-TYILG-GDRH-DN-----G-LFHIDEF

FIG. 23A





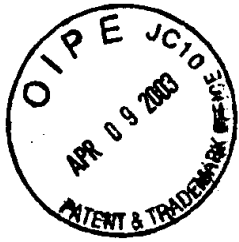
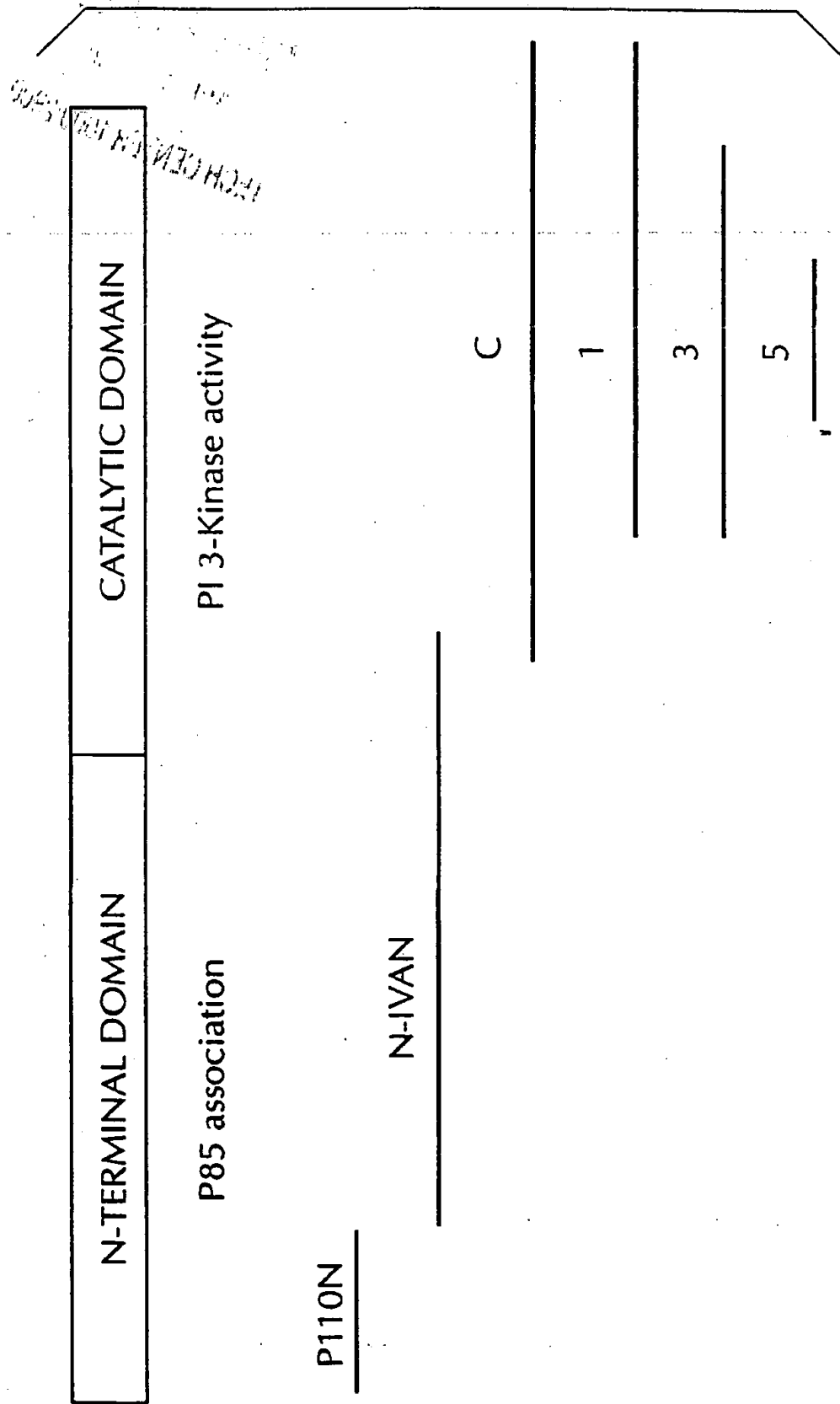


FIG. 23B



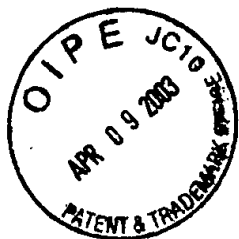
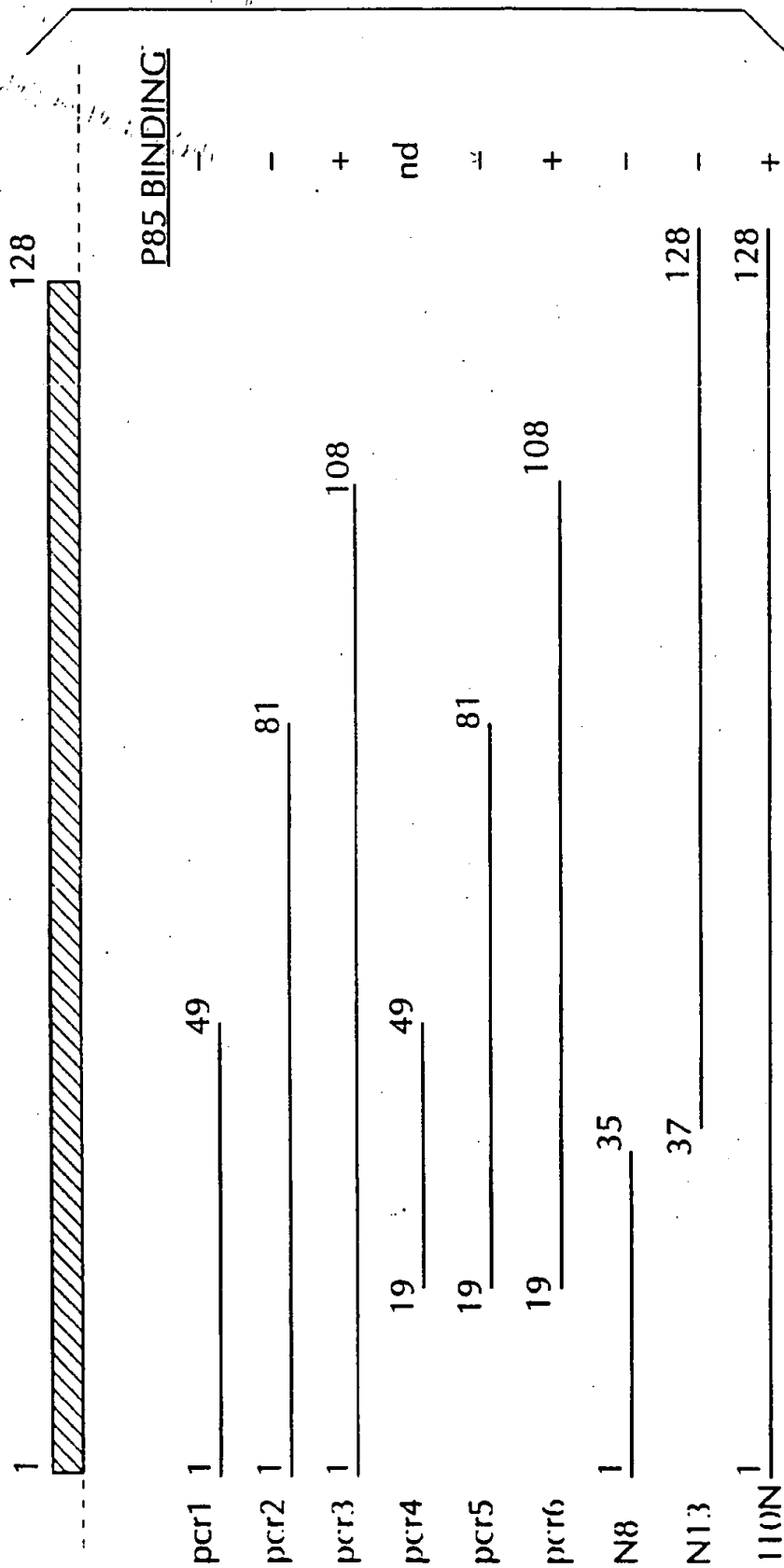


FIG. 24



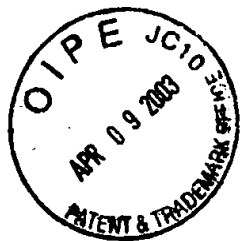
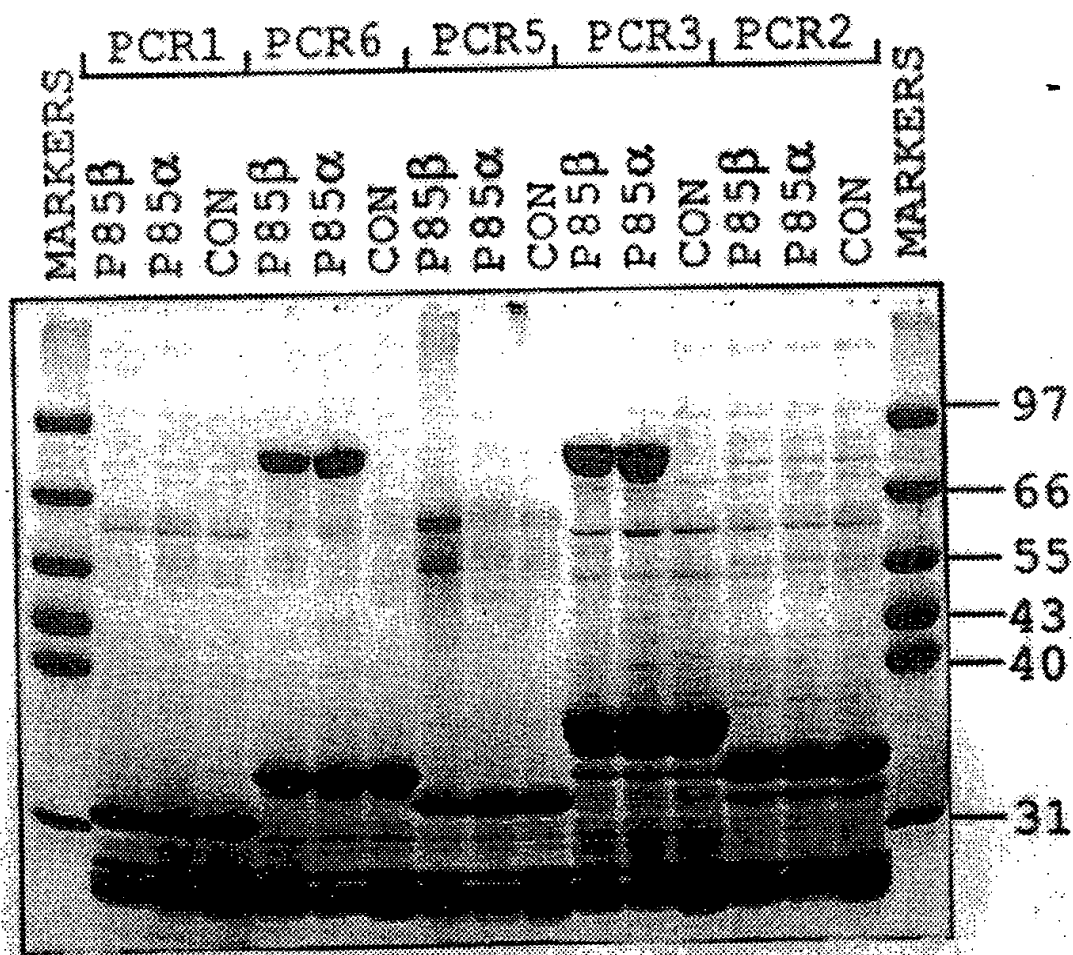


FIG. 25A



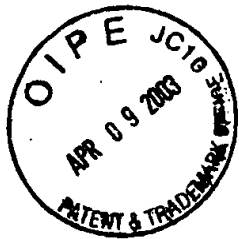


FIG. 25B

